Human G-c
Human DNA
Human G P
Human G P
Human G P
Human olf
Human GPC
Human GPC
Human GCR

Human GPC Human GPC Human G p Human GPC Human Olf

DNA encod Human GPC DNA encod Human GPC Human DNA

DNA encod

Human cDN

Human G p Human G p Human G-p

REM Olf CDN

Human

score:

Perfect

Sequence:

OM protein -

on:

Run

Scoring table:

Searched:

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Human; G-protein coupled receptor; HGPRBMY25; immune disease; inflammatory disease; arthritis; asthma; AIDS; psoriasis; graft-versus-host disease; systemic lupus erythematosus; reproductive disease; varicocele; orchitis; neural disorder; Alzheimer's disease; Parkinson's disease; depression; schizophrenia; cardiovascular disorder; hypertension; acute heart failure; pulmonary disorder; endocrine disorder; obesity; diabetes; anorexia; bone disorder; osteoporosis; pain; cancer; chromosome identification;
                   Abk68612 E
Ab277974 F
Ab277974 F
Ab277971 F
Ab377971 F
Ab31027 F
Abx68587 F
Abx68587 F
Abx68576 F
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Abk37545 I
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Aas42259 |
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Abq88355 I
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ABA81539
AAH31738
AAS42265
ABZ42976
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ABA81537
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ABA81538
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27-MAR-2001; 2001US-0278952P.
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  gene therapy; gene; ss
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                                       US2003060409-A1.
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ACD91434
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Aas42339 Human GDN
Abz43046 Human GPC
Abk37625 DNA encod
Abq88371 Human G p
Abq88372 Human G p
Acc65344 Human GPC
Aah31850 Human GPC
                                                                         August 27, 2004, 16:27:32; Search time 474 Seconds (without alignments) 2948.644 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                nucleic search, using frame_plus_p2n model
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AGCCATGTGATCCTACACACGTACTGTGAGCACATGGCTGTGGAGCTGGAGCTGGGCTGTGGA 1136
Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant; ss; food additive; cosmetic; fragrance; pharmaceutical additive.
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                                                ArgGlySerLeuLeuMetLeuProCysProPhePheIleGlyArgLeuAsnPheCysGln
                                                                                                           SerHisValIleLeuHisThrTyrCysGluHisMetAlaValValLysLeuAlaCysGlY
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24-MAR-2000; 2000US-0192033P.
12-AFR-2000; 2000US-0198474P.
26-MAY-2000; 2000US-0199335P.
25-UN-2000; 2000US-0207702P.
23-UN-2000; 2000US-0213849P.
16-AUG-2000; 2000US-0226534P.
07-SEP-2000; 2000US-0236732P.
07-FEB-2001; 2001US-0266862P.
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                                                                                                                                         New nucleic acid molecule encoding a human G-protein coupled receptor (HGPRBMY25) is useful for diagnosing, preventing or treating diseases involving the receptor, e.g. inflammation, diabetes, asthma, hypertension
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P-PSDB; ABO42809.
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GluSerThrValLeuLeuAlaMetAlaPheAspArgTyrValAlaIleCysHisProLeu 140
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                                                                                                                                                                      The invention relates to nucleic acids encoding human olfactory receptors, OR, (a g protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise and
                                                                                                                                                                                                                                                                                                                         fragrances. The present sequence encodes a human olfactory receptor of the invention
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 990 BP; 188 A; 285 C; 221 G; 296 T; 0 U; 0 Other;
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SerHisVallleLeuHisThrTyrCysGluHisMetAlaValValLysLeuAlaCysGly

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for drug development e.g. based on olfactory and gustatory receptors in form of agonists and antagonists by screening intrinsic and extrinsic ligands as bitter taste inhibitors, taste enhancers and fragrance improvers. Note: The sequence data for this patent did not form part the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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The invention relates to a method of representing sensory perception of one or more odourants. The method comprises: (a) providing a conformation of an olfactory receptors or ligand binding domains (LBD) of these receptors; (b) measuring values X1 to Xn representative of these receptors; (b) measuring values X1 to Xn representative of conformation of the LBD of at least one of the n olfactory conformation of the LBD of at least one of the n olfactory copporates, (ii) activating at least one of the n olfactory receptors with the one of more odourants; and (c) generating a colfactory receptors with the one or more odourants; and (c) generating a colfactory receptors with the one or more odourants; and (c) generating a colfactory receptors with the one or more odourants; and (c) generating a colfactory receptors with the one or more odourants; and (c) generating a colfactory receptor perception from the values X1 to Xn. The copperation of the sensory perception of odourants is useful for the design and formulation of odour and taste compositions. ABK3799-ABK37754 and ABK37921 represent human olfactory G-coupled receptor coding confounces and related PCR primers of the invention
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                                                                                                 ValTyrGlyValLysThrLysGln1leArglysArgValValArgValPheGlnSerGly
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                                 HisIleHisIleLeuLeuAlaAsnValTyrLeuLeuLeuProProAlaLeuAsnProVal
                                                  odourant;
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Li L, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P;
Smithson G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S;
Gunther E, Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM;
Zhong H, Ellerman KE, Wolenc A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ88354 to ABQ88417 represent human G protein coupled receptor (GPCR) cDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins from the present invention. GPCR sequences can have neuroprotective, nootropic, anti-HIV, antiasthmatic, antiateriosclerotic, cytostatic, immunomodulator, antiinflammatory, antidiabetic, anorectic, heemostatic, antibactic, antiulcer, antiulcer, antiallergic, hepatotropic and antiparkinsonian activities, and can be used in vaccines and gene therapy. GPCR proteins, uncleic acid molecules, and antibodies from the present invention can be used for manufacturing a medicament for treating or preventing a GPCR-associated disorder or syndrome related to cell signal processing and metabolic pathway modulation, such as cardiomyopathy, atheroscierosis, diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human G-protein coupled receptor X (GPCRX) polypeptide, useful for treating or preventing GPCRX-associated disorders e.g. diabetes, atherosclerosis, cancer or obesity.
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nootropic, anti-HVV, antiaethmatic, antiatreriosclerotic; cytostatic, immunomodulator; antiinflammatory; antidiabetic; anorectic; haemostatic, antibacterial; fungicide; protozal; virucide; nephrotropic; osteopathic; cardiant; antiulcer; antiallergic; hepatocropic; antiparkinsonian; HLVV, vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes, metabolic pathway modulation; atherosclerosis; carcer; obesity; asthma; infection; parkinson's disease; osteoporosis; carcer; obesity; asthma; allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder; systemic lupus erythematosus; gene; ss.
                                                                                                                                                                                                                                                                                             G protein coupled receptor; GPCR; GPCRX; neuroprotective;
                                                                                                                                                                                                                          Human G protein coupled receptor cDNA SEQ ID NO:35.
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10-JAN-2001; 2001US-025973P.
12-JAN-2001; 2001US-025973P.
12-JAN-2001; 2001US-026149BP.
24-JAN-2001; 2001US-026149BP.
22-FBB-2001; 2001US-0267464P.
22-FBB-2001; 2001US-0271021P.
14-MAR-2001; 2001US-027150P.
18-APR-2001; 2001US-028150P.
18-APR-2001; 2001US-028150P.
19-JUN-2001; 2001US-0285718P.
                                    ABQ88371 standard; cDNA; 998
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16-AUG-2001;
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04-JAN-2001; 2001US-0257876P.
10-JAN-2001; 2001US-0259743P.
12-JAN-2001; 2001US-0261498P.
24-JAN-2001; 2001US-0261498P.
24-JAN-2001; 2001US-0267464P.
22-FEB-2001; 2001US-0275946P.
14-MAR-2001; 2001US-0275946P.
23-MAR-2001; 2001US-0275946P.
23-APR-2001; 2001US-0284591P.
19-UUN-2001; 2001US-0284591P.
19-UUN-2001; 2001US-0289531P.
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                ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be used diagnostically to monitor protein levels in tissues as part of a clinical testing procedure such as in determining the efficacy of a given treatment regimen. ADQ88418 to ADQ8859 represent PCR primers and probes for the human GPCRs of the present invention
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          Parkinson's disease,
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Human; G protein coupled receptor; GPCRX; neuroprotective; nootropic; anti-HIV; antiasthmatic; antiarteriosclerotic; cytostatic; immunomodulator; antiinflammatory; antidiabetic; anorectic; cytostatic; antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic; cardiant; antiulcer; antiallergic; hepatocropic; antiparkinsonian; HIV; vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes; metabolic pathway modulation; atherosclerosis; cardiomyopathy; asthma; infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer; systemic lupus erythematosus; gene; ss.
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Malyankar U
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Peyman JA, Macdougall JR, Stone D, Vernet CAM, Sher
Millet I, Tchernev VT, Anderson D, Gusev V, Malyank
lerman KE, Wolenc A;
ID NO:37
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A ABO88354 to ABO88417 represent human G protein coupled receptor (GPCR) CDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins converted to the present invention. GPCR sequences can have neuroprotective, converted anti-HIV, antiasthmatic, antiatreriosclerotic, cytostatic, moutropic, anti-HIV, antiasthmatic, antiateriosclerotic, cytostatic, contibacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic, antializer, and can be used in vaccines and gene therapy. GPCR proteins, concluding a medicament for treating or preventing a GPCR cused for manufacturing a medicament for treating or preventing a GPCR cused for manufacturing a medicament for treating or preventing a GPCR cused for manufacturing a medicament for cell signal processing and especies, cancer, obesity, infections (bacterial, fungal processing and ciabetes, cancer, obesity, infections (bacterial, fungal protozoal or viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease, carchinistis, stroke, systemic lupus crythemarosus, or haematopoletic disorders. Anti-GPCR antibodies can be used diagnostically to monitor protein levels in tissues as part of a crythematoment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes xxx Claim 8; Page 88; 354pp; English.

Sequence 998 BP: 190 A:

us-10-081-775-2.rng

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The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a receptors are useful for determining the interaction pattern of a differences in the olfactory faculties of different individuals
1041 CATAITCACAITCITITGGCCAAIGITTAICIGCTITITGCCACCIGCICITAAICCGG
                     301 ValTyrGlyValLygThrLygGlnlleArgLygArgValValArgValPheGlnSerGlY
                                 New polynuclectides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                        Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour rescent profile; scent fingerprint; scent representation; ds.
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        polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of
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The invention relates to a novel human G-coupled receptor (I). (I) and its corresponding polynucleotides are useful for diagnosing, treating or preventing cell proliferative diseases (e.g. lymphoma, leukaemia, breast disease, multiple sclerosis of mental retardation), cardiovascular diseases, multiple sclerosis or amental retardation), cardiovascular failure), gastrointestinal disorders (e.g. dysphagia, indigestion or gastritis), autoimmune/inflammatory disorders (e.g. AIDS, Crohn's disease or systemic lupus erythematosus) or metabolic disorders (e.g. diabetes or parvovirus). ABK16615-ABK16637 represent novel human G-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating or preventing cell (e.g. stroke), cardiovascular
                                                                   Human; cytostatic; neuroprotective; immunosuppressant; nootropic; anti-inflammatory; anti-viral; gastrointestinal; cardiovascular; carethorotective; G-coupled receptor; cell proliferative disease; lymphoma; leukaemia; breast cancer; cirrhosis; neurological disorder; stroke; Alzheimer's disease; multiple sclerosis; mental retardation; cardiovascular disease; multiple sclerosis; mental retardation; congestive heart failure; gastrointestinal disorder; dysphagia; AlDS; gastremic lupus erythematosus; metabolic disorder; crohn's disease; systemic lupus erythematosus; metabolic disorder; diabetes; obesity; viral infection; herpesvirus; parvovirus;
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                                          Human G-coupled receptor (GCREC) cDNA, Seg ID No 42.
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proliferative (e.g. leukemia), neurological
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Au-Young J;
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autoimmune/inflammatory disorders.
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2000US-0207476P.
2000US-0208834P.
2000US-0208861P.
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02-JUN-2000; 2
02-JUN-2000; 2
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MetGluSerProHisHisThrAspValAspProSerValPhePheLeuLeuGlyIlePro

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ABK16633 standard; cDNA; 966

ABK16633;

for olfactory and pheromone G protein-coupled receptor

Human

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                                                                       121 ATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTGAACCAGTCTTGCAAGGCT
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GlyLeuGluGlnPheHisLeuTrpLeuSerLeuProValCysGlyLeuGlyThrAlaThr
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standard; DNA; 966

ABK68612 ABK68612

ABK6861

(first entry)

02-JUL-2002

The invention relates to olfactory and Pheromone G-protein coupled creeptor (GPCR) or a protein 95% identical to the GPCR, a specific active receptor (GPCR) or a protein 95% identical to the GPCR, a specific active correction and its encoding polynuclectide. Also included are an agonist, comparising the polynuclectide, a cell transformed by the vector, a noncompositing the polynuclectide, a cell transformed by the vector, a noncompositing the receptor and screening (detection and possibly, recovering) of compounds which are known or not known to be agonist, antagonists or compounds which are known or not known to be agonist, antagonists or inhibitors of natural compounds to the GPCR. The receptor-derived compination or substitution of an existing taste and/or a improvement, elimination or substitution of an existing taste and/or a fragrance of (or in) the food and/or commettion products. They can also be consect in the preparation of medicament in the treatment and/or prevention of a mammalian disorder, such as cell migration, sterility, psychotic and chaptession, depression, for promoting axonal growth, nerve cell connection and nerve regeneration for modulating male and female connection and nerve regeneration for modulating male and female. 9 Novel pheromone G-protein coupled receptor and receptor-derived agonists, ancagonists or inhibitors useful in food or cosmetic products or in the treatment or prevention of neurological disorders such as anxiety and Human; ds; gene; olfactory and pheromone G protein coupled receptor; GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic; anorectic; taste; fragrance; food additive; cometic; cell migration; eterility; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; depression; axonal growth; menstrual cycle; appetite sexual motivation; sexual attraction; prevention or the treatment by stimulation of several mammalian behaviours, such as stimulation or suppression of appetite, sexual serious sation, agraesion and for promoting or suppressing chemical communication between organisms. The present sequence is a human DNA encoding an olfactory and pheromone GPCR BP; 182 A; 276 C; 217 G; 291 T; 0 U; 0 Other; 966 317 1 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Disclosure; Page 646-647; 833pp; English. US-10-081-775-2 (1-329) x ABK68612 (1-966) 1.34e-164 1649.00 99.07% 98.75% 95.98% 22-SEP-2000; 2000EP-00870211. 21-SEP-2001; 2001WO-BE000162 2002-330013/36. Similarity: (CHEM-) CHEMCOM SA P-PSDB; AAU95725 Percent Similarity: WO200224726-A2 schizophrenia. Sequence 966 Alignment Scores: Homo sapiens 28-MAR-2002 aggression σ Veithen A; Query Match: Best Local 셤 ð

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                                     IlevalGlyAsnIleThrIleLeuValValAlaThrGluProValLeuHisLysPro
                                                                           ValTyrLeuPheLeuCysMetLeuSerThrIleAspLeuAlaAlaSerValSerThrVal
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Human; gene; anorectic; antiasthmatic; antidiabetic; hypotensive; antiparkinsonian; nootropic; neuroprotective; tranquiliser; antinflamatory; osteopathic; cardiant; neuroleptic; antiarthritic; gene therapy; olfactory G protein-coupled receptor; GPCR; infection; obesity; diabetes; hypertension; malnutrition; Parkinson's disease; Albeimer's disease; Korsakoff's psychosis; rheumatoid arthritis; chronic obstructive pulmonary disease; anxiety; osteoporosis; asthma; myocardial infarction; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel human olfactory G protein-coupled receptors (GPCR) and their coding sequences (ABZ77872-ABZ77986 and ABR01571-ABR01685). The GPCRs and coding sequences are useful for diagnosing or treating a disease or condition associated with GPCR, e.g. infections, obesity, diabetes, hypertension, malnutrition, Parkinson's disease, Alzheimer's disease, Korsakoff's psychosis, anxiety, rheumatoid arthitis, chronic obstructive pulmonary disease, osteoporosis, asthma, myocardial infarction, schizophrenia, or osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New olfactory G protein-coupled receptor gene nucleic acid and polypeptide, useful for diagnosing or treating a disease or condition associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition or Alzheimer's disease.
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   protein coupled receptor coding sequence
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
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549 CACTATGGGTCATTGCTCTCCCCAGAGTCTGTAGGCAAGCTGGGGGCTGCAGCCGTGCTT
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Conservative:
Mismatches:
Indels:
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978.50
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                                  New polynucleotide,
patient in need of
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WPI; 2003-315783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human olfactory G protein-coupled receptors (GPCR) and their coding sequences (ABZ77872-ABZ77986 and ABR01571-ABR01685). The GPCRs and coding sequences are useful for diagnosing or treating a disease or condition associated with GPCR, e.g. infections, obesity, diabetes, hypertension, malnutrition, Parkinson's disease, Alzheimer's disease, Korsakoff's psychosis, anxiety, rheumatoid arthritis, chronic obstructive pulmonary disease, osteoporosis, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New olfactory G protein-coupled receptor gene nucleic acid and by Orypeptide, useful for diagnosing or treating a disease or condition associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition or Alzheimer's disease.
                                                                                        846 AAGAGGCAAAGGCCTAAGACCTTTGGCACTTGTGGCTCCCACCTGGGTGTCATACTTCTC
LeuPheCysIleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeuSerSer
                      HisGluAlaArgSerLysAlaLeuGlyThrCysGlySerHisValCysVallleLeulle
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    or osteoarthritis
                                                            948
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Mismatches:
Indels:
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Matches:
                        BP; 187 A; 284 C; 221 G; 256
   schizophrenia,
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                                                       1.07e-90
950.50
74.75%
58.14%
55.33%
myocardial infarction,
                                                                                          Similarity:
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                       Sequence 948
                                             Alignment Scores:
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Matches:
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2000US-0184809P.
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                                                                 AAH31721 standard; DNA; 942
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73.91%
59.87%
54.22%
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Gln 318
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24-FEB-2000;
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299 ProvalvalTyrGlyValLysThrLysGlnIleArgLysArgValValArgValPhe 317
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The present sequence is one of a number of isolated polynuclectides which encode polypeptides involved in olfactory sensation. The polynuclectides can be used in screening for olfactory agonists and antagonists. The identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which receptors are useful for determining the interaction pattern of a scent composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals
                                                                                                                                                                                                                                      New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
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(YEDA ) YEDA RES & DEV
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24-FEB-2000;
 19-APR-2001
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.15e-88 931.50 73.79% 57.28% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match DB:

(1-985)US-10-081-775-2 (1-329) x AAH32052

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211 AlaHisIleGlyValAlaAlaValValArgGlySerLeuLeuMetLeuProCysProPhe 171 604 231 664 251 724 271 784 429 GGCAAGCTGGGGGCTGCAGCTTGGTGGTTTGGGACTCATGACCCACTCACCTGC 212 AlaalaLeuLeuValIleGlyValAspLeuPheCysileGlyLeuSerTyrAlaLeuile PhelleGlyArgLeuAsnPheCysGlnSerHisVallleLeuHisThrTyrCysGluHis MetAlaValValLysLeuAlaCysGlyAspThrArgProAsnArgValTyrGlyLeuThr 605 GCTGCCACACTGGTGGGCCACTGACTCCATCTGTATTGCTGTCTCTATGCACTCATCTGTC 232 AlaGlnAlaValLeuArgLeuSerSerHisGluAlaArgSerLysAlaLeuGlyThrCys GlySerHisValCysValIleLeuIleSerTyrThrProAlaLeuPheSerPhePheThr 785 CAGCGGTTTGGCCAGCACGCCCCGGCACATCCACATCCTTCTAGCTGACCTCTACCTG LeuLeuProProAlaLeuAsnProValValTyrGlyValLysThrLysGlnIleArgLys HisArgPheGlyHisHisValProValHisIleHisIleLeuLeuAlaAsnValTyrLeu 312 ArgvalvalArgValPheGlnSerGly 320 905 GGGCCCTCCGGCTTCTGAAGTGGGGC 931 192 725 272 252 292 Š g ò g $\dot{\delta}$ g à a à d ò g ð à

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geneseqn2001as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2001bs:* geneseqn2003as:* geneseqn1980s:* geneseqn1990s:* geneseqn2002s:* geneseqn2004s: geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Acd91434 Human G-p	Human	Abk37625 nna ercod		Human	Human	Human	Himan	Human	Human	Himan	7 Prohe	Himan	Probe	Human	5 Probe	Human	Himan	4 Human	1 Drope	1 Himan	· in
SUMMARIES	ACD91434	AAS42339 AB243046	ABK37625	ABQ88371	ABQ88372	ADC86344	AAH31850	ABK16633	ABK68612	ABZ77974	AAD19143	AA113897	ABA55607	AAI35262	ABA45127	ABA25305	AAK29302	AAK03835	ABS28924	AA103764	ABS03861	AAH32015
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* Query Match	100.0	4.66	99.4	99.4	99.4	99.4	96.9	96.9	6.96	80.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.0
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New nucleic acid molecule encoding a human G-protein coupled receptor (HGPRBMY25) is useful for diagnosing, preventing or treating diseases involving the receptor, e.g. inflammation, diabetes, asthma, hypertension

P-PSDB; ABO42809.

Claim 1; Fig 1A-B; 139pp; English.

or cancer

	Aad12947 Human G-n	Himan	Himph	-		_	Himan	Drobe	Himan	Aai48420 Drobe #17	Himan	Probe	Himan	Himan	Himse	Drobe		Trans.	Firman	Duman.	Liman	Aah32013 Human off
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	U 44	945	945	945	945	1345	945	945	945	945	945	945	945						1360		-	942 4
0	20.0	38.0	38.0	38.0	38.0	38.0	37.9	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.3	37.3	37.2	37.0	36.9
275	3.0	375.2	375.2	375.2	375.2	374.6	373.6	369.8	369.8	369.8	369.8	369.8	369.8	369.8	369.8	369.8	369.8	368.4	368.4	367.2	365	364
2.0	7	25	56	27	28	29	30	c 31		c 33	c 34	c 32	c 36	m	с 38	c 39	c 40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N_Geneseq_29Jan04:*

Database

Human, G-protein coupled receptor; HGPRBMY25; immune disease; inflammatory disease; arthritis; asthma; AIDS; psoriasis; graft-versus-host disease; systemic lupus erythematorsus; reproductive disorder; variacocele; orchitis; neural disorder; Alzheimer's disease; Parkinson's disease; depression; schizophrenia; cardiovascular disorder; hypertension; acute heart failure; pulmonary disorder; endocrine disorder; obesity; diabetes; anorexia; bone disorder; osteoporosis; pain; cancer; chromosome identification; Human G-protein coupled receptor HGPRBMY25 cDNA. Mintier GA; ACD91434 standard; cDNA; 1567 BP. 21-FEB-2001; 2001US-0270134P. 27-MAR-2001; 2001US-0278952P. 21-FEB-2002; 2002US-00081775. (first entry) Feder JN, (RAMA/) RAMANATHAN C S. (FEDE/) FEDER J N. (MINT/) MINTIER G A. bone disorder; osteopos gene therapy; gene; ss WPI; 2003-521919/49. US2003060409-A1. Ramanathan CS, Homo sapiens 22-SEP-2003 27-MAR-2003. ACD91434; ACD91434

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Nucleic acids encoding human olfactory G protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic
CATGAAGCTCGGTCCAAGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCATCATC 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant; ss; food additive; cosmetic; fragrance; pharmaceutical additive.
                                                                                                                                 1317 TCTTATACACCAGCCCTCTTCTCTCTTTTTACACACGCTTTGGCCATCACGTTCAGTC
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                                                                                       TCTTATACACCAGCCCTCTTCTCCTT
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24-MAR-2000; 2000US-019847P.
24-APR-2000; 2000US-019847P.
26-MAY-2000; 2000US-0199335P.
23-JUN-2000; 2000US-0207702P.
23-JUN-2000; 2000US-021849P.
16-AUG-2000; 2000US-0226534P.
07-SEP-2000; 2000US-0226534P.
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P-PSDB; AAU24646.
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                                    The invention describes an isolated nucleic acid molecule comprising a sequence that is at least 95% identical to a polynucleotide encoding novel human G-protein coupled receptor HGPRBMY25. The nucleic acid molecule, polypeptide and antibody are useful in diagnosing, preventing, treating or ameliorating medical conditions where GPCR is directly or indirectly, involved, such as immune or inflammatory diseases (e.g. arthritis, asthma, AIDS, graft-versus-host disease, psoriasis or systemic lupus erythematosus), reproductive disorders (e.g. varicocale or orchitis), neural disorders (e.g. Alzheimer's disease, pstkinson's disease, depression or schizophrenia), cardiovascular disorders (e.g. hypertension or acute heart failure), pulmonary disorders (e.g. hypertension or acute heart failure), pulmonary disorders, endocrine disorders (e.g. obseity, diabetes or anorexia), hone 
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                                                                                                                                                                                                                                                                                                                               osteoporosis), pain or cancer. The polynucleotide may also be used in chromosome identification, in identifying organisms from minute biological samples, or as molecular weight markers. This sequence encodes biological parallely.
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                                                              Length 990;
                                     Sequence 990 BP; 188 A; 285 C; 221 G; 296 T; 0 U; 0 Other;
                                                                               Indels
                                                             DB 5;
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                                                          Score 980.6; DB 5;
Pred. No. 6.5e-308;
0; Mismatches 4;
                                                        99.4%;
                                                       Query Match
Best Local Similarity 99.6
Matches 983; Conservative
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The invention relates to a method for screening G protein-coupled receptor (GPCR) genes (ABZ42870-ABZ4316) and/or GPCR proteins (ABP95596-ABP95942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene homologous with a known GPCR gene. The receptor proteins and encoded genes are useful for studying in vivo signal transduction mechanism and identifying targets for drug development e.g. based on olfactory and gustatory receptors in ligands as bitter taste inhibitors, taste enhancers and fragrance improvers. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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961 CAGGGAATGGGCATCAAGGCATCTGAG
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13-FEB-2001; 2001JP-00034434.
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The invention relates to a method of representing sensory perception of one or more odourants. The method comprises: (a) providing a representative class of n olfactory receptors or ligand binding domains (EDD) of these receptors; (b) measuring values XI to Xn representative of at least one activity of one or more odourants selected from: (i) binding one or more odourants to the LBD of at least one of the n olfactory receptors with the one or more odourants; and (iii) blocking at least one of the n olfactory receptors with the one or more odourants; and (c) generating a configuration of sensory perception from the values XI to Xn. The representation of the sensory perception of odourants is useful for the design and formulation of odour and taste compositions. ABK37499-ABK37754 and ABK37918-ABK37921 represent human olfactory G-coupled receptor coding sequences and related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                              Representing sensory perception of one or more odorants for the identification and design of tastes and odors comprises providing representative group of n olfactory receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 115; 182pp; English
                                                                                                                                        22-JUN-2000; 2000US-0213812P.
13-MAR-2001; 2001US-00804291.
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                       Score 980.6; DB 6; Length 990;
Pred. No. 6.5e-308;
0; Mismatches 4; Indels 0
Sequence 990 BP; 188 A; 285 C; 221 G; 296 T; 0 U; 0 Other;
                             99.4%;
                                                           983; Conservative
                                               Local Similarity
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odourant;

olfactory G-coupled receptor; sensory perception of composition; taste composition; gene; ss.

Homo sapiens

Human; odour

DNA encoding G-coupled olfactory receptor #127

(first entry)

08-MAY-2002

ABK37625

ABK37625 standard; cDNA; 990

RESULT 4 ABK37625

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Human; G protein coupled receptor; GPCRX; neuroprotective; nootropic; anti-HIV; antiaschmatic; antiarteriosclerotic; cytostatic; immunomodulator; antiinflammatory; antidiabetic; anorectic; nemostatic; cartiacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic; cardiant; antiuleer; antiallergic; hepatotropic; antiparkinsonian; HIV; vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes; metabolic pathway modulation; atherosclerosis; cancer; obesity; diabetes; infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer; allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder; systemic lupus erythematosus; gene; ss.
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                                                                       AGCCATGTGATCCTACACACGTACTGTGAGCACATGGCTGTGGAAGCTGGCGCTGTGGA
                                      CGCTATGCCACAATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTG
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2000US-0256635P. 2000US-0257876P. 2001US-0259743P. 2001US-0260718P. 2001US-0261498P.

04-JAN-2001; 2 10-JAN-2001; 2 12-JAN-2001; 2 18-DEC-2000; 21-DEC-2000;

18-DEC-2001; 2001WO-US049347

WO200250276-A2

27-JUN-2002

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ABQ88354 to ABQ88417 represent human G protein coupled receptor (GPCR) CC CDNA sequences, and ABP51660 to ABP31624 represent human GPCR proteins from the present invention. GPCR sequences can have neuroprotective, concertopic, anti-HIV, antiatehmatic, antiarteriosclerotic, cytostatic, immunomodulator, antialinear, antializer, antializer, hepatotropic, antipartines, and can be used in vaccines and gene therapy. GPCR proteins, activities, and can be used in vaccines and gene therapy. GPCR proteins, cardiant, antializer, and antibodies from the present invention can be nucleic acid molecules, and antibodies from the present invention can be nucleic acid molecules, and antibodies from the present invention can be used for manufacturing a medicament for treating or preventing a GPCR sesociated disorder or syndrome related to cell signal processing and metabolic pathway modulation, such as cardiomyopathy, atherosclerosis, diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or viral), HIV, asthma, Parkinson's disease, osteoporosis, crohn's disease, ulcers allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus cused diagnostically to monitor protein levels in tissues as part of a used diagnostically to monitor protein levels in tissues as part of a used diagnostically to monitor protein levels in tissues as part of a customent regimen. ABQ88418 to ABQ88639 represent PCR primers and probes treatment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes
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                                                                                                                                                                                                                         Smithson G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S; Gunther E, Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM; Zhong H, Ellerman KE, Wolenc A;
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99.4%; Score 980.6; DB 6;
Best Local Similarity 99.6%; Pred. No. 6.5e-308;
Matches 983; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 88; 354pp; English.
24-JAN-2001; 2001US-0263689P.
08-FEB-2001; 2001US-0267464P.
22-FEB-2001; 2001US-0271021P.
14-MAR-2001; 2001US-0275946P.
23-MAR-2001; 2001US-0278150P.
19-APR-2001; 2001US-0284591P.
23-APR-2001; 2001US-0284591P.
19-UUN-2001; 2001US-0285718P.
16-AUG-2001; 2001US-0299327P.
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Padigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P; on G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S; r B, Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM; H, Ellerman KB, Wolenc A;

WPI; 2002-557660/59.

P-PSDB; ABP51578

10-JAN-2001; 2001US-0260718P: 24-JAN-2001; 2001US-0261498P: 24-JAN-2001; 2001US-0261498P: 08-FEB-2001; 2001US-0267464P: 14-MAR-2001; 2001US-0271021P: 14-MAR-2001; 2001US-027194F: 23-MAR-2001; 2001US-0275946P: 18-APR-2001; 2001US-0278150P: 23-APR-2001; 2001US-028459P: 19-JUN-2001; 2001US-028459P:

2001US-0312902P

16-AUG-2001;

(CURA-) CURAGEN CORP

Li L, Padiga Smithson G,

Gunther E, Zhong H,

2000US-0257876P. 2001US-0259743P.

04-JAN-2001;

18-DEC-2001; 2001WO-US049347

27-JUN-2002

New isolated human G-protein coupled receptor X (GPCRX) polypeptide, useful for treating or preventing GPCRX-associated disorders e.g. diabetes, atherosclerosis, cancer or obesity.

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Human, G protein coupled receptor; GPCR; GPCRX; neuroprotective; nootropic; anti-HIV, antiasthmatic; antiarteriosclerotic; cytostatic; immunomodulator; antiinflammatory; antidiabetic; anorectic; haemostatic; antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic; cardiant; antiulcer; antiallergic; hepatotropic; antiparkinsonian; HIV; waccine; gene therapy; cell signal processing; cardiomyopathy; diabetes; metabolic pathway modulation; atherosclerososis, cancer; obsesty; aethma; infection; Parkinson's disease, osteoporosis; Crohn's disease; ulcer; allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder; systemic lupus erythematosus; gene; ss.
                                                                                                                                    Human G protein coupled receptor cDNA SEQ ID NO:37.
              ABQ88372 standard; cDNA; 998
                                                                                                (first entry)
                                                                                              23-SEP-2002
                                                        AB088372;
ABQ88372
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WO200250276-A2 Homo sapiens

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Contropic, anti-HIV, antiasted to ABP51624 represent human GPCR proteins confirm the present invention. GPCR agedences can have neuroprotective, from the present invention. GPCR agedences can have neuroprotective, contropic, anti-HIV, antiasthmatic, antiarteriosclerotic, cytostatic, immunomodulator, antialflammatory, antiatidabetic, anorectic, haemostatic, antibocterial, fungicide, proteozoal, virucide, nephrotropic, osteopathic, cardiant, antiulcer, antiallergic, hepatotropic and antiparkinsonian activities, and can be used in vaccines and gene therapy. GPCR proteins, nucleic acid molecules, and antibodies from the present invention can be used for manufacturing a medicament for treating or preventing a GPCR casociated disorder or syndrome related to cell signal processing and metabolic pathway modulation, such as cardiomyopathy, atherosclerosis, cancer, obesity, infections (bacterial, fungal, proteozoal or viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease, cylicars, allergiae, cirthosis, glomerulomephritis, stroke, systemic lupus crythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be collinical testing procedure such as in determining the efficacy of a given of the human of the hu
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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                      New polynucleotide, useful for preparing a composition for treatin
patient in need of increased or suppressed activity or expression
guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1390 BP; 317 A; 353 C; 293 G; 427 T; 0 U; 0 Other;
                                                                                                                 & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 797; 28pp; English
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                                                       2002EP-00013517
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                                                          18-JUN-2002;
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 Length 1390;
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Score 980.6; DB 9;
Pred. No. 7.9e-308;
0; Mismatches 4;
    99.4%;
99.6%;
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protein coupled receptor; gene therapy

guanosine triphosphate-binding

ds; gene; human; GPCR;

797 ON

SEQ ID

gene

Human GPCR

(first entry)

01-JAN-2004

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can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in the detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingarprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals
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                                                                                                                                                                                     Length 963;
                                                                                                                                                        Sequence 963 BP; 181 A; 276 C; 216 G; 290 T; 0 U; 0 Other;
                                                                                                                                                                                                             Indels
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                                                                                                                                                                                 Score 956.6; DB 4;
Pred. No. 4.1e-300;
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Matches 959; Conservative
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                           TTGTTTTGGATTGGTCTCTCTATGCCCTAATTGCACAAGCTGTCCTTCGCCTCTCATCC
                                                                                                                                                          CATGAAGCTCGGTCCAAGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATC
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       AGCCATGTGATCCTACACACGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGA
                                                        GACACCAGGCCTAACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; olfactory receptor; OR; primary scent determination;
secondary scent determination; polypeptide library; odour receptor;
scent profile; scent fingerprint; scent representation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               olfactory receptor polynucleotide, SEQ ID NO: 423
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or viral infections (e.g. infection by herpesvirus or s). ABK16615-ABK16637 represent novel human G-coupled

parvovirus) obesity),

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The invention relates to a novel human G-coupled receptor (I). (I) and its corresponding polynucleotides are useful for diagnosing, treating or preventing cell proliferative diseases (e.g. lymphoma, leukaemia, breast cancer or cirrhosis), neurological disorders (e.g. stroke, Alzheimer's disease, multiple sclerosis or mental retardation), cardiovascular diseases (e.g. atherosclerosis, angina pectoris or congestive heart failure), gastrointestinal disorders (e.g. dysphagia, indigestion or gastritis), autoimmune/inflammacory disorders (e.g. AlDS, Crohn's disease or systemic lupus erythematosus) or metabolic disorders (e.g. diabetes or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New G-protein coupled receptors useful for treating or preventing cell proliferative (e.g. leukemia), neurological (e.g. stroke), cardiovascular or autoimmune/inflammatory disorders.
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                   GTTTATCTGCTTTTTGCCACCTGCTCTTTAATCCTGTGGTATATGGAGTTAAGACCAAACAG
                                                                                      Lu Y;
 GTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; neuroprotective; immunosuppressant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffin JA,
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Au-Young J;
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25-MAY-2000; 2000US-0207476P.
02-UUN-2000; 2000US-0208834P.
07-UUN-2000; 2000US-0208861P.
                                                                                                                                                                                                                                                    ABK16633 standard; cDNA; 966
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Kallick DA,
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Pred. No. 4.1e-300;
0; Mismatches 4;
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The invention relates to olfactory and Pheromone G-protein coupled receptor (GPCR) or a protein 95% identical to the GPCR, a specific active portion and its encoding polymucleotide. Also included are an agonist, antagonist or inhibitor of the GPCR or the polymucleotide, a vector. Comprising the polymucleotide, a cell transformed by the vector, a non-human mammal comprising a partial or total deletion of the polymucleotide encoding the receptor and screening (detection and possibly, recovering) of compounds which are known or not known to be agonist, antagonists or inhibitors of natural compounds to the GPCR. The receptor-derived agonists, antagonists or inhibitors of natural compounds to the GPCR. The receptor-derived agonists, inhibitors or compounds are used as an improvement, elimination or substitution of an existing taste and/or a fragrance of (or in) the food and/or cosmetic products. They can also be used in the preparation of medicament in the treatment and/or prevention of a mammalian disorders, such as cell migration, sterility, psychotic and neurological disorders, including anxiety, schizophrenia, manic connection and nerve regeneration for modulating male and female endocrine functions, hormone production and the menstrual cycle, for the prevention or the treatment by stimulation of several mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel pheromone G-protein coupled receptor and receptor-derived agonists, antagonists or inhibitors useful in food or cosmetic products or in the treatment or prevention of neurological disorders such as anxiety and schizophrenia.
                                                                                                                                                                                                                                          Human DNA for olfactory and pheromone G protein-coupled receptor #212
                                                                                                                                                                                                                                                                                                        GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic; anorectic; taste; fragrance; food additive; cosmetic; cell migration; sterility; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; depression; axonal growth; menstrual cycle; appetite sexual motivation; sexual attraction;
                                                                                                                                                                                                                                                                                          ds; gene; olfactory and pheromone G protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        behaviours, such as stimulation or suppression of appetite, sexual motivation, sexual attraction, aggression and for promoting or suppressing chemical communication between organisms. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suppressing chemical communication between organisms. The present sequence is a human DNA encoding an olfactory and pheromone GPCR
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Sequence 966 BP; 182 A; 276 C; 217 G; 291 T; 0 U; 0 Other;

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atherosclerosis, diabetes; cardiant; cytostatic; cancer; obesity; pain; diabetes mellitus; anorexia; cachexia; cardiowyopathy; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorders; retinal disorder; HIV;
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                      GACTTGGCTGCCTCTGTCTCCAAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G-protein coupled receptor 12 (GPCR12) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New olfactory G protein-coupled receptor gene nucleic acid and polypeptide, useful for diagnosing or treating a disease or condition associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel human olfactory G protein-coupled receptors (GPCR) and their coding sequences (ABZ77872-ABZ77996 and ABR01571-ABR01685). The GPCRs and coding sequences are useful for diagnosing or treating a disease or condition associated with GPCR, e.g. infections, obesity, diabetes, hypertension, malnutrition, Parkinson's disease, Alzheimer's disease, Korsakoff's psychosis, anxiety, rheumatoid arthritis, chronic obstructive pulmonary disease, osteoporosis, asthma, myocardial infarction, schizophrenia, or osteoparthritis
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                                                                                                                                                                                          Human G protein coupled receptor coding sequence SEQ ID 205.
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Pred. No. 3.2e-246;
); Mismatches 50;
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06-NOV-2001; 2001US-0332758P
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                                                           ABZ77974 standard; DNA; 948
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Best Local Similarity
...-hes 821; Conservative
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                  RESULT 11
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CATGTACCTCTTTCTGGCCATGTTGGCAGCCATGGACCTGGTCCTTTCCTCCTCAGCACT
                                                              GGCACATATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACTGTGCTACTGGCCAT
                                                                                                                                                                                                                                                                                                                                                        434 GTCCCTCATCACCAAGATTGGCATGGCTGCTGTGGCCCGGGCCTGTGACACTAATGACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTGAAACCAGTCTTGCACAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-Protein coupled receptor polypeptides and NAs useful for preventing, diagnosing and treating cardiomyopathy, atherosclerosis, cancers and diabetes.
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E, Casman SJ, Lepley DM, Gangolli
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                                                                                                       /*tag= c
/product= "Mature GPCR12 protein"
                       "Human GPCR12 protein"
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28-DEC-2000; 2000US-0258511P.
28-DEC-2000; 2000US-0258828P.
04-JAN-2001; 2001US-0259659P.
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14-AUG-2000; 2000US-0275226P.
1-BEG-2000; 2000US-025639P.
18-DEG-2000; 2000US-0256524P.
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2000US-0199960P.
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Macdougall JR, Smithson G;
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15..179
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P-PSDB; AAE11906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
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APPLICANT: Harlocker, Steven G.
APPLICANT: Rede, Steven G.
APPLICANT: Reter, Mark
APPLICANT: Rales, Michael
APPLICANT: Roles, Michael
APPLICANT: Roles, Michael
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APPLICANT: Roles, Michael
APPLICANT: OMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENITON: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.42708
FURBERY APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
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US-09-465-901-17

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60.2%; Pred. No. 1.6e-99;
iive 0; Mismatches 365
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
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nes 553; Conservative
       TYPE: DNA
CORGANISM: Homo sapiens
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Pred. No. 1.6e-99;
0; Mismatches 365; Indels
           CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
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Matches 553; Conservative
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                 390 CCATGCTGCAGTGCTCAACAATACAGTAACAGCCCAGATTGGCATCGTGGCTGTGGTCCG
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526, Application US/09636215
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Patent No. 6620922
GENERAL INFORMATION:
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183 AGGCTCCCTGCTCATGCTCCCATGTCCCTTCTTTATTGGGCGTTTGAACTTCTGCCAAAG 542
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR INUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: STUART & OLSTEIN
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ZIP: 07068

ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"WEDTITER: IBM PC compatible
""""FR: PC-DOS/MS-DOS
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; Patent No. 5756309
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REFERENCE/DOCKET UNBER: 32:
TELECOMMUNICATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
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CITY: Roseland
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ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,1
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COUNTRY: USA
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TILE REPERBNCE: 210121.427221
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEC ID NOS: 898
SOFTWARE: FREESEQ for Windows Version 3.0
SEC ID NO 526
LENGTH: 963
TURGH: 963
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Pred. No. 1.6e-99;
0; Mismatches 365; Indels
                                                                                                                                                                                   Sequence 526, Application US/09685166A
Patent No. 6630305
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                               963 GGGAATGGGCATCAAGGC 980
                                                                          TGACAAGGACTTGCAGGC 947
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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ilarity 60.2%;
Conservative
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                                                                                                                                                                US-09-685-166A-526
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APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HDRAJ70
NUMBER OF SEQUENCES: 8
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Pred. No. 2.4e-98;
0; Mismatches 367;
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Patentin Release #1.0,
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APPLICATION NUMBER: US/09/053,303
                                                                                                                                                     1203 TGACAAGGACTTGCAGGC 1220
                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09053303
Patent No. 5948890
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STUART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FERTATO, GREGOLY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.5%;
60.0%;
                                                                                   963 GGGAATGGGCATCAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 201-994-1700
201-994-1744
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Best Local Similarity 60.0°
Matches 551; Conservative
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274..1233
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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APPLICANT: Soppet
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LOCATION:
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US-09-053-303-1
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                                LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        0.6 Query Match
Best Local Similarity 60.0 Matches 551, Conservative
SEQUENCE CHARACTERISTICS:
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274..1233
                                                                                                                                                                   MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                          linear
                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-465-980-1
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             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/053,303
APPLICATION NUMBER: 09/053,303
FILING DATE:
ATRONEY/AGENT INFORMATION:
ATRONEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                     NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
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Matches 551; Conservative
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STRANDEDNESS: single
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US-09-339-115-1
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APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09339115; Patent No. 6372891
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CITY: Roseland
STATE: New Jersey
COUNTRY: USA
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ADDRESSEE: CARELLA, E
ADDRESSEE: STUART & C
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COMPUTER READABLE FORM:
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Pred. No. 2.4e-98;
0; Mismatches 367;
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Best Local Similarity 60.0
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PCT-US95-07093-1
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GARELLA, BYRNE, BAIN, GILFILLIAN, CECCHI,
ADDRESSEE: STUART & OLGTEIN
STREET: 6 Becker Farm Road
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
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APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-UGN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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STATE: New Jersey
COUNTRY: USA
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LOCATION:
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AAAGCTCTGAGTACCTGTGGCTCCCACATGGCATCATCCTGGTTTTTCTACATCCTGCC 1356
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1237 ATTTCCTATGGCTTTATCCTCCATGCAGTCTTTCACCTTCCATCTCATGATGCCCAGCAC 1296
                                                                                                                                                                                                                                                                                796 CICITCICCITITITACACACCGCITIGGCCATCAC---GITCCAGICCAIAITCACAIT 852
                                                                                                                                                                                                                                                                                                                                                                                     CTITIGGCCAAIGITTAICIGCTITIIGCCACCIGCICTIAAICCIGIGGIAIAIGGAGIT 912
                                                                                                                                                                                 676 CTCTCCTATGCCCTAATTGCACAAGCTGTCCTTCGCCTCTCATCCCATGAAGCTCGGTCC
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Patent No. 650038
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%; Score 142.4; DB 4; Length 1854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
RAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFRERNCE/DOCKET NUMBER: PA-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: sing
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CALIFORNIA
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US-09-016-434-1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-016-434-1312
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 326.2; DB 4; Length 1539;
Pred. No. 8.1e-97;
0; Mismatches 343; Indels 3;
                                                                                                                            APPLICANT: Liu, Cheraga.com
APPLICANT: Zhou, Pind
APPLICANT: Zhou, Vind
APPLICANT: Zhang, Jie
APPLICANT: Mang, Jia
APPLICANT: Wang, Jian-Rui
APPLICANT: Wa, Aidong J.
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
ITILE OF INVENTION: POLYPeptides
FILE REFERENCE: 190C1P25
FILE REFERENCE: 190C1P26
CURRENT APPLICATION NUMBER: US/09/668,680
FILE REFERENCE: 2000-09-22
PRIOR PELING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,167
PRIOR APPLICATION NUMBER: 09/540,167
PRIOR APPLICATION NUMBER: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PL_Genes Version 2.0
SEQ ID NO 13
LENGTH: 1539
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                                                                                         Tang, Y. Tom
Liu, Chenghua
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; LOCATION: (130)..(1539)
US-09-668-680-13
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ORGANISM: Homo sapiens
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Best Local Similarity
                  Sequence 13, Applica
Patent No. 6436703
GENERAL INFORMATION:
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                               Indels
     Pred. No. 2.6e-36;
0; Mismatches 371;
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TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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49.2%; Pred. No. 8.9e-35;
iive 0; Mismatches 395
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-109-1995
CLASSIFICATION: 435
                                                                                                                                                                                   APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 7494
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
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MOLECULE TYPE: DNA (genomic)
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nucleic acid
EDNESS: double
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SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
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                                                                                                                                                                                                                                    FILING DATE: 08 CLASSIFICATION:
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Matches 389;
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                                                                                                                                                                                                              438 CACTGACACCATCATTGCCCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCTGCTCAT 497
306 TIGIGCCICACAGAIGTICTICTICAIATICTITGGIAIAACIGAGIGCIGCCIAITIGGC 365
                                                                       378 GGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACTCCGCTATGCCACAATCCT 437
                                                                                                                                          366 AGCCATGGCCTTTGACCGCTATATGGCTATATGTTCCCCCACTCCACTATGCAACCCGAAT
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APPLICANT: Romett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
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APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION
TELEPHONE: 312-616-5600
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STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                  839
                                                                                                                                                      858 GGCCAATGITIATCTGCTTTTGCCACCTGCTTTAATCCTGTGGTATATGGAGTTAAGAC 917
                                                                                                                                                                                                                         840 GGCCCTCTTCTACACAGTAGTGACATCCATGCTGAACCCTATCATCTATAGTTTAAGGAA 899
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                                                                                  786 TATTACCTATTTGAGGCCCAAGTCTAGCCA-----CTCACCAGGAATGGACAATTCTT
           798 CTICTCCTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTT
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APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 05-NOV-1995
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49.6%; Pred. No. 1.8e-33;
rative 0; Mismatches 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATE: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08748506 Patent No. 6159707 GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
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: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                        900 CAAGGAAGTC 909
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MOLECULE TYPE:
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Pred. No. 1.4e-32;
0; Mismatches 400; Indels
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INPORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
TREFRENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                       ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
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SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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116..1003
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STRANDEDNESS: both
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Best Local Similarity
Matches 371; Conserv
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LOCATION:
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US-08-467-948A-1
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                                                                                                                                                                 Length 966;
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UNMBER OF SEQUENCES; 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   Indels
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I: 1100 NEW YORK AVE., NW, SUITE 600
WASHINGTON
                                                                                                                                                     Score 131.8; DB 3;
Pred. No. 5.3e-33;
0; Mismatches 330;
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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Patent No. 5998164
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                     Query Match 13.4%;
Best Local Similarity 49.8%;
Matches 328; Conservative
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CAO, LIANG
NI, JIAN
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APPLICANT: LI, YI
APPLICANT: CAO, LII
APPLICANT: NI, JIAH
APPLICANT: GENTZ, I
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APPLICANT:
APPLICANT:
   ; TOPOLOGI:
; MOLECULE TY
US-08-748-506-6
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Length 1713;

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STATE: IL COUNTRY:
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US-08-748-506-8
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                                                                                                                       CCCATGAAGCTCGGTCCAAGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCTCA 778
                                                                                                                                                     CTGGGGAGGGCCGCAGAAAGGCCTTCTCCACCTGCTCCTCCCACCTCTGCGTAGTGGGAC 872
GAGACACCAGGCCTAACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTG 658
                           CTGATACCTGGCTCAACCAGGTGGTCATCTTTGAAGCCTGCATGTTCATCCTGGTGGGAC 752
                                                                                         CACTCTGCCTGGTGCTGGTCTCCTACTCACACATCCTGGGGGGCATCCTGAGGATCCAGT
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APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: BULT, CAROL J.
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: SUTTON III, GRANGER G.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 131; DB 3; Length 17
Pred. No. 1.4e-32;
0; Mismatches 400; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUFTWARE: PC-DOS/MS-DOS
SUFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
APPLICATION: 435
APPLICATION: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: STERNE, KESSLER, GOLDSTEIN & FOX 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08467947A Patent No. 6090575 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
13.3%;
Best Local Similarity 48.1%;
Matches 371; Conservative (
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US-08-467-947A-1
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CTGTCTTCTTCCTGGGGCATCCCAGGTCTGGAACAATTTCATTTGTGGGCTCTCACTCC 118
                                                                              153 CAGAGTTCCTCCTACTGGGATTTCTCCTGGGCCCAAGGATTCAGATGCTCCTCTTTGGGC 212
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STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Job time : 96 secs

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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.8%; Score 126.8; DB 3;
Best Local Similarity 49.5%; Pred. No. 2.3e-31;
Matches 326; Conservative 0; Mismatches 332;
               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION ATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION UNMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY AGAPT: INFORMATION:

REFERENCE DOCKET NUMBER: 74940
TELEFAX: 312-616-5600
TELEFAX: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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; MOLECULE TYPE: DNA (genomic)
US-08-748-506-8
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Search completed: August 27, 2004, 18:30:17

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 27, 2004, 16:19:27; Search time 540 Seconds (without alignments) 8995.273 Million cell updates/sec US-10-081-775-1_COPY_537_1523 987 OM nucleic - nucleic search, using sw model Perfect score: Sequence: Run on:

1 atgtccagcactcttggcca.....tgggcatcaaggcatctgag IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

3237270 seqs, 2460713050 residues Searched:

Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

| Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* Published Applications NA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 1, Appli Sequence 262, App Sequence 353, App Sequence 35, Appl Sequence 37, Appl Sequence 923, Appl Sequence 797, Appl Sequence 797, Appl Sequence 25, Appl Sequence 879, Appl Sequence 879, Appl Sequence 90, Appl Sequence 90, Appl Sequence 90, Appl Description US-09-804-291-262 US-09-804-291-262 3 US-10-343-850A-353 5 US-10-025-806-37 5 US-10-025-806-37 6 US-10-025-806-37 7 US-10-292-798-797 1 US-09-844-861A-25 US-10-17-161-879 US-09-864-761-3771 US-09-866-055-90 Query Match Length DB Score 980.6 980.6 980.6 980.6 980.6 980.6 376.2 376.2 375.2 Result No.

US-09-804-291-90

Sequence 25. Appl	161	Sequence 5. Appli	Sequence 757. App	Seguence 161 App	Sequence 20537. A	Sequence 25, Appl	Sequence 947, App		21.	Sequence 877, App	755	163	19.	86.		12	9	Sequence 96. Appl	31	159	315	157	93,	945	819	23	34	36.	833	-
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIBE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR, HGPRBMY25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES
FILE REFERENCE: D0126 NP
CURRENT APPLICATION NUMBER: US/10/081,775
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,134
PRIOR FILING DATE: 2001-03-27
PRIOR PELING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 69
SOFTWARE PATENTIN VERSION 3.0
SSQ ID NO 1
LENGTH: 1567
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US-10-081-775-1; Sequence 1, Application US/10081775; Publication No. US20030060409A1
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Best Local Similarity 100.
Matches 987; Conservative
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US-10-081-775-1
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ORGANISM: homo sapiens
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596 61 GICTICTICCTCCTGGGCATCCCAGGICTGGAACAATTICATTTGTGGGCTCTCACTTCCT 120 537 AIGICCAGCACTCTIGGCCACACAIGGAAICICCTCAICACACGIGAIGTIGACCCTICI 1 AIGICCAGCACTCTIGGCCACAACATGGAATCTCCTCATCACACTGATGTTGACCCTTCT ð a ð a

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US-09-886-055-262
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APPLICANT: STRYER, LUBERT
APPLICANT: ZOZULYA, SERGEY
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: DISCENSORS OF CHEMICAL SENSANTS
PILE REPERRINCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886,055
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'Sequence 262, Application US/09886055

; Patent No. US20020132273A1

; GENERAL INFORMATION:
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Pred. No. 2.3e-305;
); Mismatches 4;
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 262
LENGTH: 990
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Publication No. US20040067499A1
GENERAL INFORMATION:
APPLICANT: HAGA, TATSUTA
ITILE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR PILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SEQ ID NO 353
LENGTH: 990
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ORGANISM: Homo sapiens
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US-10-343-650A-353
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US-10-343-650A-353
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841 CATAITCACAITCITITGGCCAATGITIAICTGCTITITGCCACCTGCTCTTAAICCIGTG
                                901 GTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGG
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                                                                                                                                                                                                                                    ; Sequence 262, Application US/09804291
; Bublication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
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Pred. No. 2.3e-305;
0; Mismatches 4;
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CURRENT PAPLICATION NUMBER: US/09/804,291
CURRENT FILING DATE: 2001-03-13
PRIOR PRILOR PLING DATE: 2001-03-13
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 60/199,335
PRIOR APPLICATION NUMBER: 60/199,335
PRIOR APPLICATION NUMBER: 60/20,702
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-3
PRIOR FILING DATE: 2000-06-3
PRIOR FILING DATE: 2000-06-3
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
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PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2011-02-07
NUMBER OF SEQ ID NOS: 529
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                                                                                                                                 99.4%;
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Best Local Similarity 99.6
Matches 983; Conservative
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US-09-804-291-262
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US-09-804-291-262
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LENGTH: 990
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APPLICANT: Scilore, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Mactowall, John
APPLICANT: Macougall, John
APPLICANT: Stone, David
APPLICANT: Stone, Corine
APPLICANT: Stone, Corine
APPLICANT: Guncher, Erik
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Maderson, David
APPLICANT: Macrian, Valizar
APPLICANT: Macrian, Waldimir
APPLICANT: Macrian, Waldimir
APPLICANT: Macrian, Waren
APPLICANT: Malency Haibong
APPLICANT: Ellerman, Karen
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CURRENT FILING DATE: 2001-12-19
PRIOR PAPLICATION NUMBER: 00/256, 635
PRIOR PILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-06-19
PRIOR PRILING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-24
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-03-24
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PRIOR PELING DATE: 2001-03-15
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PRIOR PELING DATE: 2001-03-18
PRIOR PELING DATE: 2001-03-18
PRIOR PELING DATE: 2001-03-18
US-10-025-806-35
; Sequence 35, Application US/10025806
; Publication No. US20030198955A1
; GENERAL INFORMATION:
                                                                                                                                            APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rekuda, Ramesh
APPLICANT: Colman, Steven
APPLICANT: Spytek, Kimberly
APPLICANT: Gasman, Stacie
APPLICANT: Gasman, Stacie
APPLICANT: Garlach, Valenit
APPLICANT: Garlach, Valenit
APPLICANT: Sciore, Paul
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ORGANISM: Homo
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; LOCATION: (2)
US-10-025-806-35
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Sequence 37, Application US/10025806 Publication No. US20030198955A1 GENERAL INFORMATION: APPLICANT: Li, Li
                                                                     Padigaru, Muralidhara
Ballinger, Robert
Kekuda, Ramesh
Colman, Steven
Spytek, Kimberly
Casman, Stacie
Edinger, Shlomit
Gerlach, Valerie
Sciore, Paul
Smithson, Glennda
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ORGANISM: Homo sapiens
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APPLICANT: PENGLAND.
APPLICANT: PRAGOUGALI, John
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APPLICANT: PRAGOUGALI, John
APPLICANT: STATE, COILE
APPLICANT: STATE, COILE
APPLICANT: Guncher, Erik
APPLICANT: Maloungli, Sureel
APPLICANT: Milet, Isabelle
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Length 998;

DB 15;

99.4%; Score 980.6;

Query Match

RESULT

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99.4%;
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Best Local Similarity 99.6
Matches 983; Conservative
                                                                                                                                                                                                                                                                    , NAME/KEY: CDS
, LOCATION: (201)..(1166)
US-10-017-161-923
                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    NAME/KEY: source
LOCATION: (1)..(1366)
                                                                                                                                                                             SEQ ID NO 923
LENGTH: 136
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RESULT

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Fublication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUNA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ARIVATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED REC
FILE REFERENCE: 084355/0152
CURRENT PAPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOSTWARE PETENTIN VOR: 2.1 601 g ð

321 GTGTGTGGCTTAGGCACACCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCC 380	181 ACTGAACCAGTCTTGCACAAGCCTGTGTACCTTTTCTGTGCATGCTCTCAACCATCGAC 240	241 TIGGCIGCCICTGTCICCACAGITCCCAAGCIACTGGCTAICTICIGGIGIGGAGCCGGA 300	301 CATATATCTGCCTCTGCCTGGCACATATGTTCTTCATTCA	361 GAGICCACIGIGCIACIGGCCIIGGCCIIIGAICGCIACGIGGCCAICIGCCACIC 420 	421 CGCTATGCCACAATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTG 480	481 CGAGGCTCCCTGCTCATGCTCCCATGTCCCTTTTATTGGGCGTTTGAACTTCTGCGA 540	541 AGCCATGTGATCCTACACGTACTGTGAGCACATGGCTGGGTGAAGCTGGCCGGCC	601 GACACCAGGCCTAACCGTGTGTATAGGCCTGACAGCTGCACTGTTGGTCATTGGGGTTGAC 660	661 INGITINGCAINGCICICICIANGCCCTAATICACAAGCIGICCITCGCCTCTCAICC 720	721 CATGAAGCTCGGTCCAAGGCCCTAGGGACCTGTGGTTCCCATGTGTGTCATCCTCATC 780	781 TCTTATACACCAGCCCTCTTCTCCTTTTTACACACCGCTTTGGCCATCACGTTCCAGTC 840	841 CATATTCACATTCTTTTGCCCAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTG 900	901 GTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGG 960 	961 CAGGGAATGGGCATCAGG 987 	RESULT 9 US-10-297-021-42 Sequence 42, Application US/10297021 Sequence 42, Application No. US20040023294A1 GENERAL INPORMATION: APPLICANT: INVETE GENOMICS, INC. APPLICANT: TRIBOULEY, Caherine M. APPLICANT: TRIBOULEY, Caherine M. APPLICANT: TRIBOULEY, Caherine M. APPLICANT: TRIBOULEY, Caherine M. APPLICANT: TRIBOULEY, Caherine M. APPLICANT: TRORNYO, Michael APPLICANT: THORNYO, Michael APPLICANT: KALLICK, Deborah A.
qq	& g	Qy	Qy	Qy	Qy	Qy Dp	Sy Dp	& g	95 PP 65	& A	& g	S G	\$ g	ò qa	RESULT US-10 Seque PEDED PEDED APPE APPE APPE APPE APPE AP
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APPLICANT: Casman, Seacuse
APPLICANT: MacDougail, John
APPLICANT: MacDougail, John
APPLICANT: Smithson, Glennda
FITLE OF INVENTION: No. US20030216304Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-789 US
CURRENT FILING DATE: 2001-04-27
FRICK PILING DATE: 2001-04-27
FRICK PILING DATE: 2000-04-27
FRICK PILING DATE: 2000-08-14-28
FRICK FILING DATE: 2000-08-14-39
FRICK FILING DATE: 2000-12-18
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Pred. No. 2.7e-110;
0; Mismatches 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 25, Application US/09844861A; Publication No. US20030216304A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Spytek, Kimberly
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Best Local Similarity 62.7%;
Matches 585; Conservative
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Alsobrook, John
Gangolli, Esha
Casman, Stacie
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Grosse, William
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APPLICANT:
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APPLICANT: GANDHI, Ameena R.
APPLICANT: AU-YOUNG, Janice
TILE OF INVENTION: G-ROTTEIN COUPLED RECEPTORS
FILE PERERENCE: STE-0781 PCT
CURRENT APPLICATION NUMBER: US/10/297,021
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/206,222; 60/207,476; 60/208,834; 60/208,861; 60/209,868
PRIOR APPLICATION NUMBER: 60/206,222; 60/207,476; 60/208,834; 60/208,861; 60/209,868
PRIOR FILING DATE: 2000-05-22; 2000-06-02; 2000-06-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PERL Program
SEQ ID NO 42
LENGTH: 966
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; OTHER INFORMATION: Incyte ID No. US20040023294A1 7476077CB1
US-10-297-021-42
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Pred. No. 1.3e-297;
0; Mismatches 4;
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Best Local Similarity 99.6
Matches 959; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED REG; FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1145)
US-10-017-161-879
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NAME/KEY: source
LOCATION: (1)..(1345)
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                                                                                                                                  CATGTCAGCCTCCAATATCACCTTAACACATCCAACTGCCTTCTTGTTGGTGGGGATTCC
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                                                  Gaps
      Length 1345;
Query Match
38.1%; Score 376.2; DB 15; Length
Best Local Similarity 62.7%; Pred. No. 3.2e-110;
Matches 585; Conservative 0; Mismatches 348; Indels
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Sequence 879, Application US/10017161 Publication No. US20030143668A1 GENERAL INFORMATION: APPLICANT: SUWA, MAKIKO APPLICANT: ASAI, KITOSHI APPLICANT: AKIYAMA, YUTAKA APPLICANT: ARIYAMA, YUTAKA APPLICANT: ABURATANI, HIROYUKI

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N: MAP TO ACO10930.2

N: EXPRESSED IN LUNG, SIGNAL = 2.3

N: EXPRESSED IN BONE MARROW, SIGNAL = 2

N: EXPRESSED IN BRAIN, SIGNAL = 1.7

N: EXPRESSED IN PLACENTA, SIGNAL = 2.3

N: EXPRESSED IN PLACENTA, SIGNAL = 3

N: EXPRESSED IN BT474, SIGNAL = 1.8

N: EXPRESSED IN HEART, SIGNAL = 2.8

N: EXPRESSED IN HEART, SIGNAL = 2.8

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
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Pred. No. 3.9e-110;
0; Mismatches 348;
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Best Local Similarity 62.7%;
Matches 585; Conservative 0
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Db 541 TGTGAACACATGGCTGTGGGGGGTGGGGGACACTAGCTTCAACAATATCTAT 600 Qy 625 GGGCTGACAGCTGTTGGTCATTGGGGTTGGGGTTTGCATTGCATTGCTCTCTAT 684	Db 661 APCTTATTCTCAGGCATTCTACTCTTCAGGAGGCCCCTACAGGAGGCATT 720 Qy 745 GGGACCTGGTGTTCTCTGTTCTCTTCTTCTTCTC 804	RESULT 14 US-09-804-291-90 i Sequence 90, Application US/09804291 i Fublication No. US2003008059A1 i GENERAL INPORMATION: APDLICANT: 2021LA, SERGEY i TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME FILE REFREENCE: P 0.79805 i CURRENT FILIAND DATE: 2001-03-13 i FRIOR APPLICATION NUMBER: 60/192,033 FRIOR APPLICATION NUMBER: 60/192,033 FRIOR PILING DATE: 2000-03-14 i FRIOR APPLICATION NUMBER: 60/192,033 FRIOR PILING DATE: 2000-04-14 i FRIOR PILING DATE: 2000-04-14 i FRIOR PILING DATE: 2000-05-26 i FRIOR PILING DATE: 2000-05-3 i FRIOR FILING DATE: 2000-6-3 i FRIOR FILING DATE: 2000-6-3 i FRIOR PILING DATE: 2000-6-3 i FRIOR PILING DATE: 2000-6-3 i FRIOR FILING DATE: 2000-6-3 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR FILING DATE: 2000-6-16 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR APPLICATION NUMBER: 60/266,862 i FRIOR FILING DATE: 2000-08-16 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR FILING DATE: 2000-08-16 i FRIOR APPLICATION NUMBER: 60/226,534 i FRIOR FILING DATE: 2001-02-07 i FRIOR APPLICATION NUMBER: 60/286,862 i FRIOR FILING DATE: 2001-02-07	Query Match 38.0%; Score 375.2; DB 10; Length 945; Best Local Similarity 62.7%; Pred. No. 5.6e-110; Anatches 584; Conservative 0; Mismatches 348; Indels 0; Gaps 0; Qy 25 ATGGAATCTCTCATCACATGATGATGATCTTCTTCTTCTTCTTCTTCTTCTTCTCTCCTGGGATTCCA 84
QY 864 IGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGGTATATGGAGTTAAGACCAAACA 923 Db 246 ITTCTATCTGCTCTTCCCACCCATGGTCAATCCCATAATCTATGGTGTCAAGACAAGCA 187 QY 924 GATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAG 956 Db 186 AATCCGTGAGAGAGTTTCCAAG 154	RESULT 13 US-09-886-055-90 is Sequence 90 Application US/0986055 is Patent No. US2002013273A1 is GENERAL INFORMATION: APPLICANT: STRYER, LUBERT APPLICANT: ZOZULYA, SERGE ITILE OF INVENTION: RECEPTOR FINCERPRINTING, SENSORY PERCEPTION, AND TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS FILE REFERENCE: 078003-0277150 CURRENT APPLICATION NUMBER: 05/277150 CURRENT FILING DATE: 2001-06-22 FRIOR APPLICATION NUMBER: 60/213,812 FRIOR FILING DATE: 2000-06-22 NUMBER OF SEQ ID NOS: 522 SOFOTHOR OF DATE: PATENTIN VET: 2.1	TYPE: DNA 1945 19	Qy 445 ACCATCATTGCCCACATAGGGCAGCTGTAGTGCCGAGGCTCCTGCTCCTGGTCCCCA 504 Db 421 TCCCTCATCACCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACCTCAATGACTCCA 480 Qy 505 TGTCCCTTCTTTATTGGGCTTTGAACTTCTGCCAAAGCCATGTGATCCTACACGCTAC 564 Db 481 CTCCCTTCCTGCTGAGATTTCCACTACTGCCGAGGCCCAGTGATCGCTAC 540 Db 482 CTCCCCTTCCTGCTGAGATGTTTCCACTACTGCGGAGGCCCAGTGATCGCTAC 540 Qy 565 TGTGAGCACATGGCTGTGGTGAAGCTGGCGAGCCCCAGTGTGTAT 624

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Pred. No. 5.6e-110;
0; Mismatches 348;
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US-10-182-822A-25
                         60/182,045
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL PROGram
SEQ ID NO 25
LENGTH: 945
                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 62.7%;

Matches 584; Conservative 0
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Publication No. US20030211493A1
GENERAL INFORMATION:
APPLICANT: INCTE GENOWICS, INC.; BAUGHN, Mariah R.;
APPLICANT: INCYTE GENOWICS, INC.; BAUGHN, Mariah R.;
TITLE OF INVENTION: G-FROTEIN COUFLED RECEPTORS
FILE REFERENCE: PI-0032 USN
CURRENT FILING DATE: 2001-02-01
PRIOR PAPLICATION NUMBER: US/10/182,822A
PRIOR FILING DATE: 2001-02-01
PRIOR PLING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: US 60/180,093
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SUMMARIES

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Research, 320 Charles Street, Cambridge, MA 02141, USA
Si (bases 1 to 185330)
Si Inten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barra,N., Bastien,V., Balom,T., Boguslavkiy,L., Boukhgaleer,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,P., Dearellano,K., Dewar,J., Collymore,A., Farzo,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Farzo,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Rorton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Lowine,R., Lindblad-Toh,K., Liu,G., MacLean,C., MacGonald,P., Major,J., Marlaw,V., Murphy T., Naylor,J., Marso,J., Millor,R., Norbu,C., Norman,C., Norbu,C., Norman,C., Norbu,C., Norman,C., Retea,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Schauber,B., Sthupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Viel,R., Zimmer,A. and Zody,M.
Direct Submission
                        Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 14, 2002 this sequence version replaced gi:21426295.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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center: Mitchead Institute/ MIT Center for Genome Research
Center code: WIP WW-seq.wi.mit.edu
Web site: http://www-seq.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. On the the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1. .120991
/note="assembly_fragment
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99.7%; Score 983.8; DB 2;
Best Local Similarity 99.8%; Pred. No. 2.6e-287;
Matches 985; Conservative 0; Mismatches 2;
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154022. .185330
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
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121092. .132589
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PC A61P43/00,C07K14/705,C07K16/28,C07K19/00,C12N1/15,C12N1/19, PC
                                                                                                                                                                                                                                                                                                                    PAT 17-JAN-2003
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PN JP 2002112793-A/177
PD 16-APR-2002
PD 16-APR-2003
PP 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE
PC
C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC
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840
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PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
PC Novel G-protein coupled receptors
FH Key (1)...(990).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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               170057 ICTTATACACCAGCCCTCTTCTCCTTTTTACACACCGCTTTGGCCATCACGTTCCAGTC
                                                                                170117 CATATTCACATTCTTTTGGCCAATGTTTATCTGCTTTTTGGCACCTGCTCTTAATCCTGTG
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                                                                  CATATICACATICITITGGCCAAIGITIAICIGCITTITGCCACCIGCICTIAAICCIGIG
                                                                                                                                   GTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGG
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Pred. No. 1.3e-286;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 990)
Haga.T., Takeda.S. and Miyake,N.
Novel G-procein coupled receptors
Patent: JP 2002112793-A 177 16-APR-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PP 2002112793-A/177
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                     CAGGGAATGGGCATCAAGGCATCTGAG 987
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JP 2002112793-A/177.
Homo sapiens (human)
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Best Local Similarity 99.6%;
Matches 983; Conservative
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BD144452
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AUTHORS
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                   /clone="RP11-589G14"
/clone_lib="RPCI-11 Human Male BAC"
1. .70426
/note="assembly_fragment
                                                                                                                                                                                                                                                                                        99.7%; Score 983.8; DB 2;
99.8%; Pred. No. 2.7e-287;
iive 0; Mismatches 2;
                                                                                                                   70527...78730

/note="assembly_fragment"

7831...137440

/note="assembly_fragment"

137541...203352_fragment

/note="assembly_fragment

clone=end:T7

vector_side:right"
                                                                                     Best Local Similarity 99.8
Matches 985, Conservative
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// mol_type="unassigned DNA"
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2. ..391
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RGSLLMLPCPFLICRLNFCQSHVILHTYCEHMAVVTCAGDTRPNRVYGLTAALLVIG
VDLFCIGLSYALSAQAVLELSHERRSKALGCTCGSHVCVILLSYTPALFSFFTHRFGH
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Patent: WO 0250276-A 35 27-JUN-2002,
Curagen Corporation (US)
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Best Local Similarity 99.6
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
Genome-wide discovery and analysis of human seven transmembrane
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Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 797 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
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tive 0; Mismatches 4;
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Catarrhini, Hominidae, Homo.
                1101 GTATATGGAGTTAAAGACCAAACAGATCCGTAAAAGAGTTGTGTCAGGGTGTTTCAAAGTGGG
GTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA.
On Sep 1, 2000 this sequence version replaced gi:9838305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 19 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; 04
Sequencing vector: plasmid; 04
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165996 bases at least Q40
Consensus quality: 165626 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 171387; sum-of-contigs
Quality coverage: 4.33 in Q20 bases; sum-of-contigs
Quality coverage: 4.82 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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Center project name: H_NH0658K18
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Mammalia, Eutheria, Primates,
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Waterston, R.H.
                                                                       CAGGGAATGGGCATCAAGGCATCTGAG
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HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
HOMO sapiens
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Waterston, R.H.
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GTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAASVGTVPKLLAIFWCGGHJ
SASACLAQMFFTHAFCMMESTVLLAMPDRYVAL CHPLKYATILTDTIIAHIGVAAVV
RGSLLMLPCPFLIGELHTTYCEHHAVVKLAGDFRFNKVGLTAALLVIG
VDLFCTGLSYALSAQANFLSSHFARSKALGTGGSHVCVILISYTPALFSFFTHFFGH
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7 4	ATGLICAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCT 8	9408
Sy Ob	61 GICTICTICCICCIGGGCAICCCAGGICTGGAACAAITICATITGIGGCICTCACICCCT 12	20 93 48
λ̈́o	21 GIGIGIGGCTIAGGCACCACAATIGIGGGAATATAACTATICIGGTIGTIGTIGCC 1	0
qq	7 GTGTGTGTTTAGGCACACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGTT	1288
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	241 TTGGTGGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTG	228
7 음	89227 TIGGCTGCCTCTGTCTCCAAGCTACTGGCTATTCTTCTGGTGTGGAGCCGGA 89	168
λ	CCTTCTGCATGATG 36	0
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λα	ACAATCCTCACTGACACCATGATTGCCCACATAAGGGGTGGCAGCTGTAGTG 48	0
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	41 AGCCATGTGATCCTACACGCTGTGAGCACATGGCTGTGGTGAAGCTGGCTG	0
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	601 GACACCAGGCCTAACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGAC 66	0
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	661 TIGITINGCATIGGICTCTCTATGCCCTAAITGCACAAGCIGICCTTCGCCTCCGTCC 72	0
.,	07 TIGITITIGCATIGGICICCCTATGCCCTAAGIGCACAAGCTGTCCTTCGCCTCTCATCC 88	748
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~	CICCIIIIIIACACACGCTIIGGCCAICACGIICCAGIC 88	628
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~	67 GTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTGTT	808
	961 CAGGGAATGGGCATCAAGCATCTGAG 987	
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Direct submission

Submitted (10-May-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Sesarch, 320 Charles Street, Cambridge, MA 02141, USA

Sirren, B. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N. Bastien, V. Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Rerreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Gord, S., Gord, C., Lamorette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Johnson, R., Johnson, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLen, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Micoarthy, M., McEwan, P., McKernan, R., Maldrim, J., Mathews, C., Micoarthy, M., McEwan, P., McKernan, R., Maldrim, J., Mathews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., O'Neil, D., O'Neil, D., O'Neil, D., O'Saman, S., Savery, P., Spencer, B., Sancos, R., Schauer, S., Schupback, R., Stause, N., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viane, M., Willey, R
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lackoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad, Toh, K., Liu, G., MacCean, C., MacGonald, P., Major, J., Maldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Noyen, C., Micol, R., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Faynond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severt, P., Spencer, B., Santos, R., Schauers, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Waman, D., Ye, W.J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M., Zenbek, L., Zimmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Zahnoun, J., Zenbek, L., Zimmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Simmer, A. and Zody, M., Subramanian, M., Subramanian, M., Subramanian, Subramanian, Subramanian, Subramanian, Subramanian, M., Subramanian, M., Subramanian
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
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775. 880
/rpt_aniy="(TTCC)n"
1179. 1224
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Web site: http://www-seg.wi.mit.edu
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Direct Submission

Submitted (25-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

(bases 1 to 176597)

Birran, B. Linton, L., Nusbaum, C., Lander B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chang, C., Campoplano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farceriar, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gindes, S., Gord, S., Goyette, M., Iliev, I., Johnson, R., Jones, C., Kamae, A., Kartasa, A., Kartasa, A., Kartasa, A., Kartasa, A., Martasa, M., Mille, C., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norbu, C., Norbu, C., Norman, C.H., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Rosetti, M., Royla, Santos, R., Schauer, S., Schupback, R., Sterauss, N., Subramanian, A., Talamas, J., Tesefaye, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tesefaye, S., Theodore, J., Viell, N., Voy, A., Wilson, B., Yan, R., Schauer, S., Schupback, Staman, S., Severy, P., Spencer, B., Stanger-Thoman, N., Viell, N., Voy, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Submission

Linton, J., Zembek, L., Zimmer, A. and Zody, M.

Shirrent, B., Linton, L., Nubbaum, C., Lander, E., Ali, A., Allen, N., Buiretted, Ila-AfR-2002) Whitehead Institute/MIT Center for Genome Subrassion

Shirrent, B., Linton, L., Nubbaum, C., Lander, E., Ali, A., Allen, N., Buiren, B., Birrent, B., Linton, L., Boukhgalter, B., Brown, N., Baschen, V., Boom, T., Boukhgalter, B., Stown, N., Boom, T., Collins, S., Collymore, C., Chararo, B., Choppell, Y., Colangelo, W., Collins, S., Collymore, C., Chararo, B., Choppell, Y., Colangelo, W., Collins, S., Collymore, Collins, S., Chararo, B., Choppell, Y., Colan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 176597)
                                                                                                                                             AC116156 176597 bp DNA linear PRI 13-MAY-2º
Homo sapiens chromosome 11, clone RP11-44D14, complete sequence.
AC116156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-44D14 Unpublished
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JOURNAL
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VERSION
KEYWORDS
SOURCE
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TITLE
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AUTHORS
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                                                                                                     RESULT 9
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Qy 181 ACTGAACCAGTCTTSCACAAGCCTGTGTACCTTTTCTGTGCATGCACCATCGAC 240 Db 159089 ACTGAACCATCTTGCACAGCCTGTGTACCTTTTCTGTGCATGCTTCTGCACCTTGGAC 159030 Qy 241 TGGCTGCCTCTGCACAGTTCCCAGCTACTTGTGGTGGAGCCGA 300 Db 159029 TGGCTGCTGCTCCACAGTTCCCAGCTACTTCTGGTGGAGCCGA 300 Db 159029 TGGCTGCTGCTGCTGCCTGGCTACTTCTTCTGGTGGAGCCGA 158970 Qy 301 CATATATCTGCCTGCCTGCCTGCCTGCCTGCACATATGTCTTCATTCA	<u>σ</u> 6	158729 158729 601 158669 661 158609	OY 781 TCTTATACACCAGCCCTTTTTTACACACCCGCTTTGGCCATCAGGTC 840 158489 TCTTATACACCAGCCCTCTTTTTTACACACCGCTTTGGCCATCAGGTC 158430 OY 841 CATATTCACATTCTTTTGGCCAATGTTTATCACACCGCTTTGGCCATCAGGTC 158430 Db 158429 CATATTCACATTCTTTTTGGCCAATGTTTATCTGCACTTGCACTTGGCGTCTTGGTG 900 158429 CATATTCACATTCTTTTTGGCCAATGTTTATCTGCACTTGTCACTTTTGGCGTCTTTAATCCTGTG 900 OY 901 GTATATGGAGTTAAGACCAAACAGATCGTATTTTTGCCACCTGCTCTTTAATCCTGTG 158370 OY 902 GTATATGGAGTTAAGACCAAACAGATCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGG 960 Db 158369 GTATATGGAGTTAAGACCAAACAGATCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGG 158310 QY 961 CAGGGAATGGGCATCTGAG 987 Db 158309 CAGGGAATGGGCATCTGAG 987	RESULT 10 AX241675 LOCUS DEFINITION Sequence 423 from Patent W00127158. AZ241675 AZ2
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QY 925 ATCCGTAAAAGAGTTGTCAAGGTGTTTCAAAGTGGGCAACGGCATCAAGGCATCT 984 Db 901 ATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGGGCAGGGATCGGCATCAAGGCATCT 960 QY 985 GAG 987 Db 961 GAG 963	MATHERS MATHERS AND MATHERS AND MARTHERS MATHE	505 TGTCCCTTCTTATTGGGCGTTTGAACTTCTGCCAAAGCCATGTGATCCTACACGTAC 1
Digiscents (US); YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) Location/Qualifiers 1963 forganism="synthetic construct" /mol_type="unassigned DNA" /db xref="taxon:32630" /note="(H389272 nucleotide)"	Ouery Match Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 99.64; Pred. No. 2.70-279; Best Local Sinilarity 90.64; Pred. No. 2.70-279; Best Canada	Qy 865.GTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAACAG 924

Oy 25 ATGGAATCTCCTCATCACACTGATGTTGACCCTTCTGTCTTCCTCCTGGGCATCCCA 84 Db 1 ATGGAATCTCCTAATCACACTGATGTTGACCCTTCTGTCTTCTTCCTCGGGCATCCCA 60 Qy 85 GGTCTGGAACAATTTGATTTGTGGCTCTCACTCCCTGTGTGGCTTAGGCACACCACACAATTTGATTTGATTTGATTCACTCCCTGTGTGGGCTTAGGCACACCACAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTGATTTGATTTGA	Db 61 GGTCTGGAACAATTCATTTGTGGCTCTCACTCCTGTGTGTG	OY 205 GIGTACCTITITICIGIGGECTGATCCACCACGACCIGGCTGCTCTGTCTCCACGTT 264 181 GIGTACCTITITICIGIGGAIGCTCTCAACCATGGCTGCCTCTGTCTCTCACAGTT 240	Oy 265 CCCAAGCTACTGCTATCTTCTGGTGTGGACAGATATATCTGCCTGC	Qy 325 GCACATAIGTICTICATTCATGCCTICTGCATGAGGCCTGTGCTACTGGCCATG 384	Qy 385 GCCTTTGATGGTGGCGATCTGCCACTCCGCTATGCCACAATCCTCACAC 444.	A45 ACCATGATGCCCACATAGGGGTGGCAGGCTGCAGGCTCCCTGCTCATGCTCCCA 504	Qy 505 TGTCCCTTCTTATTGGGCGTTTGAACTTCTGCCAAAGCCATGTGATCCTACACACGTAC 564	Oy 565 TGTGAGCACATGGCTGTAAGCTGCTGTGGAGACACCAGGCCTAACCGTGTGTAT 624	QY 625 GGGCTGACAGGCTGCATTGGGGTTGGCTTTGCATTGCAT	GCCCTA 	745 GGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATATACACCAGCCTCTTCTC 80	Qy 805 ITTITIACACACGCTITIGGCCATCAGTICCAGTCCATAITCACATTCTTITIGGCCAAI 864	Qy 865 GTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGATTAAGACCAAACAG 924	GCATCT 98	985 GAG 987	Db 961 GAG 963	RESULT 13 AC109341/c LOCUS AC109341 DEFINITION Homo sapiens chromosome 11, clone CTD-2504M7, complete sequence.
Qy 565 TGTGAGCACATGGCTGTGGTGAAGCTGGCTGTGGAGACACCAGGCCTAACCGTGTGTAT 624 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 601 GGGCTGACAGCTGCACTGTTGGTCATTGGGTTGACTTGTTTGCATTGGTCTCTCTATT 660 QY 685 GCCCTAATTGCACAGCTGCCTTCGCCTCTCATCCATGAAGCTCGATCGA	745 GGGACCTGTGGTTCCATGTCTGTCATCCTCATTATACACCAGCCTCT 721 GGGACCTGTGGTTCCCATGTCATCTCTTATACACCAGCCCTCT 721 GGGACCTGTGGTTCCCATGTTCTTGTTCTATCTTATACACCACCCTCTCTTATACACCACCCCTCTCTTGTTGTATCATCTTTTATACACACCACCTCTTATACACACCACCCTCTTATACACACCAC	CAAT 86	92	CATCT CATCT		RESULT 12 A4448757	LOCUS MX448757 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 MX44877 M	Homo sapiens (human) Homo sapiens	Eukaryota; metazoa; Chordata; Craniata; Ver Mammalia; Butheria; Primates; Catarrhini; H CE 1 RS Veithen,A.	TITLE OLFACTORY and pheromones g-protein coupled receptors JOURNAL Patent: WO 0224726-A 423 28-MAR-2002; FEATURES ChemCom S.A. (BE) FRATURES 1.0cation/Qualifiers	80	.	/ W_XTELE"G1:4189/858" / Ab_xref="REWTERBEL:CAD37694" / LTAINS At ion="MESPNHTDDPSVFFLIGIPGLEQFHLWLSLPVCGLGTATIVGN ITILVVVNTEPVLHKPVYELCMLSTIDLAASVSTVPKTLAIFWGGAGHISASATIAO	MFIHAFCMMESTVLLAMAFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLF CPELIGRINARCOSHVILHTYCEHMAVVKLAGGDTRRNRYGLTAALLIUTUTUTGTGL SYALSAOAVIRLSSHRAR KRAIGTMCGSHVVIIISVTDAILSERFWHDEGHUNDATIIT	•	Query Match 96.9%; Score 956.6; DB 6; Length 966; Best Local Similarity 99.6%; Pred. No. 2.7e-279; Matches 959; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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6517_.3995
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456. .6697
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Camporiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dear, K., Dear, J., Dodge, S., Faro, S., Gorder, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gorde, P., Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Mardon, P., Mardior, J., Marquis, N., Matthews, C., McCarthy, M., Mardon, P., Mardion, J., Marquis, N., Matthews, C., McCarthy, M., Mardon, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Resta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rostetl, M., Roy, A., Santos, R., Schauer, S., Schuber, S., Schuber, S., Schuer, S., Schuber, S., Schuer, S., Schuer, S., Schuer, S., Schuer, J., Vola, N., Vola, M., Travis, N., Trajilio, J., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Sody, M., Santos, M., Travis, N., Tr
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Clangelo, M., Collins, S., Collymore, A., Cook, P., DeAtellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S., Giord, S., Goyette, M., Grand-Pierre, N., Gardyna, S., Hagos, B., Horton, L., Hullew, M., Lilev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
                     AC109341.7 GI:20564454
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                                                                         Homo sapiens (human)
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Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trisillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G., Lett, Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 14, 2002 this sequence version replaced gi:20429487.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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243. 263
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/rpt family="L1PAl3"

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/db_xref="taxon:9606"
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240 CTTGGCTGCCTCTGCCACAGTTCCCAAGCTACTGCCTATCTTCTGGTGTGGAGCCGG 5932	RESULT 14 AC147586 LOCUS
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Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTGTGGCCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCC
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                        Center,
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Submitted (18-DEC-2003) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
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Best Local Similarity 89.6%; Pred. No. 3.8e-238;
Matches 884; Conservative 0; Mismatches 103; Indels
                                                                                                                                                               Center: NIH Intramural Sequencing Center Center code: NISC
Who site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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/mol_type="genomic DNA"
/db_xref="taxon:30611"
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/note="assembly_fragment
clone_end:SP6
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Center clone name: 553F22
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                                                                           2 (bases 1 to 181386)
Green, E.D.
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HTGS.PHASE2; HTGS.DRAFT.
Otolemur garnettii (small-eared galago)
Sukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metheria; Primates; Strepsirhin; Galagonidae; Otolemur.
E (bases 1 to 239335)
Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Han, J., Hangen, N., He, S.-L., Hu, P., Hurle, B., Idol, J., R.,
Karlins, E., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C.,
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Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contignable has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                   Submitted (11-SEP-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 239335)
                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-OCT-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Oct 17, 2003 this sequence version replaced gi:34576313.
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This sequence will be replaced by the finished sequence as soon as it is available and
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    .239335
forganism="Otolemur garnettii"
/mol_type="genomic DNA"
/db_xref="taxon:30611"

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Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                             NISC Comparative Sequencing Initiative
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/clone="CH256-105A13"
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Search completed: August 27, 2004, 17:37:04 Job time : 4178 secs

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AY410598 Homo sapi
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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//nol_type="genomic DNA"
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AY401472 948 bp DNA linear GSS 12-DEC-2003 Homo sapiens HCM0902 gene, VIRTUAL TRANSCRIPT, partial sequence, genemic survey sequence.

AY401472. GI:39757461
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.

(Bases 1 to 948)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Adams, M.D. and Cargill, Neng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, Neng, Control of the numan-chimp-mouse orthologous
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Submission
Submission (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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Pred. No. 1e-85;
0; Mismatches 360;
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/organism="Homo sapiens"
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/locus_tag="HCM0902"
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61.3%;
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Kockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
1. .948
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CATGTATCTCTTTCTGGCCATGCTGGCTACCACTGACCTTGTCCTGTCCTCCTCCACACA
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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RESULT 3 AY410600

JOURNAL TITLE

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948 bp DNA linear GSS 12-DEC-2003 Pan troglodytes HCM0902 gene, VIRTUAL TRANSCRIPT, partial sequence, AX401473
                                                                                                      860 CTCCCATGCTCAACCCCATCATTAATGGAGTTAGAACCAAACAGAATCGGGCACAGGGTTA 919
                                                 CACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTG 940
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1 (bases 1 to 948)
Clark, A.G., Glamowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferritera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GTGCTGGGAAACATGGTGGTGCTGCTAGTGGTACATTCAGAGCCTGTATTGCACCAGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAAACTCATAAACCATAGCCATCAGAACCCAACCTCCTTTCTGCTCATGGGAATTCCA 60
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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    .948
    /organism="Pan troglodytes"

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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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(Lase, B. to 97).

(Lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargiil, W. White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
               GCCCAGATGTTCTTTATCCATGGCTTCTCAGCTGTAGAATCTGGTATATGTAGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTACCTGGTTGTGCCACCCATGCTCAACCCCATCATCTATGGCATGAAGACCAAACAG
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and order them based on alignment.
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                                                                                                                                                                                                                                                                                                                   DB 29; Length 957;
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                                                                                                                                                                                                                                                                                                                   Score 331.2; DB 29;
Pred. No. 8e-82;
0; Mismatches 348;
                                                                                                                                  1. .v. /
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/organism="Homo gapiens"
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                                                                                                 Location/Qualifiers
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Yokohama,

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/note="unnamed protein product; OLFACTORY RECEPTOR MOR18-2 (SPTR|AAL60674, evidence: FASTY, 100%ID, 100%length, match=960)
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                                        Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Ri Genomic Sciences Center and Genom Exilon. Univision of Experimental Animal Research in Riken contributed t
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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Pred. No. 1.8e-80;
0; Mismatches 375;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 565-573 (2002)
6 (bases 1 to 1964)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                        882 TCTCTATGGAGCTAGAACCAAGGAGATTCGGAGTCGACTTCTAAAACTGCTTCACCTGGG
900 GGTATATGGAGTTAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTGTTTCAAAGTGG
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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B. Adachi, J. Alizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramco, K., Haraka, T., Hiracane, T., Hayatsu, J., Ishi, Y., Itch, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itch, M., Komo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Musa, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, M., Nakamura, M., Saski, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, T., Takau-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegger:iken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.riken.go.jp, Text. Http://genome.gsc.r
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Itegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation
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(SPTR|AAL60674, evidence: FASTY, 100%ID, 100%length,
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Please visit our web site for further details.
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/db_xref="FANTOM_DB:4631413D08"
/db_xref="MGI:2390376"
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Location/Qualifiers
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/protein_id="BAC25966.1"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 500 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (1BBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Halt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Halt, Rai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
Barrymple, B.P. and Tellam, R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ACCATCTCCACAGAGCGCTCCCTGCATAAGCCCATGTTCCTGCTGCTTGGCATGCTGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCTATTCCTTTCTCTTCCATGTACTTTGTCACCATCCTGGGGGACTGCACCATCCTCTTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MbcHereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                                                                                                                          CC500683 822 bp DNA linear GSS 1'
CH240.338N7.TARBAC13P2 CHORI-240 Bos taurus genomic clone
CH240.338N7, genomic survey sequence.
CC500683
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61.5%; Pred. No. 5.2e-77;
                                                                        2061 GATCAGCTGTGACAAGGACATTGAAGC 2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_338N7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="CHORI-240"
                           954 AAGTGGGCAGGGAATGGGCATCAAGGC
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Seg primer: SP6
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1. .822
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/cell_type="Blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Rob Holt
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JOURNAL
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IHTLSAIESTILLAMAFDRYVAICHPLRHAAVLNNTVTVQIGMVALVRGSLFFFPLPL
LIKRLAFCHSVULSHSYCVHQDVMKLAYTDTLDHVVVGLTAILLVMGVDVMFIGLSYF
LIIRTVLQLPSKSTRAKAFGTCVSHISVVLAFYVPLIGLSVVHRFGNSLDPIVHVLMG
DVYLLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDIEBAGGNT"
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                                                                                                                                                                                                                                         Length 3410;
                                                                                                                                                                                                                                  Score 327; DB 11; Length 3
Pred. No. 2.4e-80;
0; Mismatches 375; Indels
                                                                                                                    /note="putative"
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ilarity 59.5%;
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Matches 552;
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Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 GCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATGGTCTATCTTATCTACCGCCTAC
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 936)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Ferriera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.
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                                             ACCATCGACTTGGCTGCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTGGTGT
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6 6 6 6 6 6	8 6 8 6 8 6 8 6	66666666	RESULT 13 AY401480 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FUBNEE AUTHORS AUTHORS
QY 830 ACGTTCCAGTCCTATTCACATTCTTTGGCCAATGTTTATCTGCTTTTGCCACCTGCTC 889 Db 1	AY414227 AY414227 BEFINITION Mus musculus HCM5153 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION AY414227 AY414227.1 GI:39770189 SCRENCE Mus musculus GGS. Mus musculus CRGANISM Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. TITLE IIILE LILE	JOURNAL Science 1102 REFERENCE 2 (Asses 1 to 954) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, ROCKVILLE, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering This sequence was made by sequencing genomic exons and ordering FRATURES Location/Qualifiers Location/Qualifiers SOURCE / Organism="Mus musculus" // AD 7106-1 # 1	gene (1>954 /locus_tag="HCM5153" Query Match Best Local Similarity 59.6%; Pred. No. 31.2%; Score 307.8; DB 29; Length 954; Best Local Similarity 59.6%; Pred. No. 31.2%; Indels 3; Gaps 1; Matches 538; Conservative 0; Mismatches 362; Indels 3; Gaps 1; QY 65 TCTTCCTCGGGCATCCCAGGCTGGAACATTTCATTTGTGGCTCTCACTCCCTGTGT 124

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CH240_356B15.T7 CHORI-240 Bos taurus genomic clone CH240_356B15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the Plate: 356 row: B column: 15
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Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Unpublished (2003)
                                                                 876 TTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAACAGATCCGTAAAAG 935
                                                                                       849 CALTCCICCTCCCTCCATCATTACAGIGIGAGAACAAAGAGAGAAAAAGAGAACA 908
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
      789 TCGATTTGGACACAACATTCCACATTCTTGTTGCTACATCTTGGT
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/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2:
Hereford bull In Domino 99375; CHORI-240 Bovine P
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z
Tel: 604-877-6815
Fax: 604-877-6276
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Pred. No. 1.9e-72;
0; Mismatches 272; Indels 0;
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/strain="breed: Hereford"
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                            TCATCACACTGATGACCCTTCTGTCTTCTTCCTGGGCATCCCAGGTCTGGAACA
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REFERENCE 2 (bases 1 to 900) AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Noveville, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers Source /organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism="Homo sapiens" // Organism=#CM3943"	Query Match 29.8%; Score 294.4; DB 29; Length 900; Best Local Similarity 58.0%; Pred. No. 1.88-71; Natches 520; Conservative 0; Mismatches 376; Indels 0; Gaps 0; QY 25 ATGGAATCTCCTCACCACGAGGTTGACCTTCTTCTTCTTCTTCCTTACGGCATCCA 84 Db 1 ATGCCATCCTTCAACCAGAGTATTTCCACCCTGCAGCTTCTTCTTACTTA		
	TGTGAT TGTGAT TGTGAT TGGGC CAGGCC CAGGCC TTGCAT TGCAT		AY410595 AY410595 AY410595 AY410595 BDEFINITION Homo sapiens OR51C3P gene, VIRTUAL TRANSCRIPT, partial sequence, BEFINETION GENOMIC SURVEY SEQUENCE. ACCESSION AY410595. AY410595. Homo sapiens (human) GSS. SOUNCE Homo sapiens (human) ORGANISM Homo sapiens (human) AY410595. Homo sapiens (human) CRGANISM Homo sapiens (human) AY410595. AMMMalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE I (bases I to 900) AUTHORS Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous JOURNAL Science 302 (5652), 1960-1963 (2003)

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Search completed: August 27, 2004, 18:28:39 Job time : 3097 secs

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AX55971 Canis fam
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USTPTO spool/1/USION081775/runat_20082004_170213_11126/app_query.fasta_1.519
-Q=/cgn2_1 /USTPTO spool/1/USION081775/runat_20082004_170213_11126/app_query.fasta_1.519
-DB=GenEmbl -QFMT=fastap -SUFFIX=xep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -EMD=-1 -MATRIX=bloaum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -START=1 -EMD=-1 -MATRIX=DONESON_0 - MALICH=120 -MAXLEN=2000000000
-USR=-USR-GEQUERY -NGG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NGG SCORES=0 -WAIT -LOOPCLOG -LONGLOG
-NGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                             ; Search time 4663 Seconds
(without alignments)
3058.087 Million cell updates/sec
                                                                                                                                                                                                                                               1 MSSTLGHNMESPHHTDVDPS.....RKRVVRVFQSGQGMGIKASE 329
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                        nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                         3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               August 27, 2004, 17:37:09
                                                                                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Homo sapi Novel G-p Sequence

AC124272

SOURCE

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Sequencing vector: Plasmid, n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 184674 bases at least Q40 Consensus quality: 184934 bases at least Q30 Consensus quality: 184980 bases at least Q20 Insert size: 180000; agarose-fp Insert size: 185030; sum-of-contigs Quality coverage: 19.6 in Q20 bases; sum-of-contigs Quality coverage: 19.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120991: contig of 120991 bp in length 121091: gap of 100 bp 132589: contig of 11498 bp in length 132689: gap of 100 bp 153921: contig of 21232 bp in length 154021: gap of 100 bp 185309: contig of 31309 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="RPCI-11 Human Male BAC"
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154022. .185330
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Center project name: L27346
Center clone name: 607 K 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .120991
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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121092. 132589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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Universe summission

Submitted (14-JUN-2022) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (Dases 1 to 18530)

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1 Satien, V., Blonder, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Blonder, E., Choepel, Y., Colymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Rartes, P., FitzGerald, M., Gage, D., Galagan, J., Rondon, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Iliu, G., MacLean, C., Macdonald, P., Mardow, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Micol, R., Matthews, C., Murphy, T., Naylor, J., Micol, R., Matthews, C., Roman, C., Phunkhang, P., Pierre, N., Raymon, C., Micol, R., Norbu, C., Norman, C., Roman, J., Roy, A., Schauer, S., Schuback, R., Steaman, S., Semaen, S., Schuback, R., Steaman, S., Semaen, S., Schuback, R., Steaman, S., Semaen, S., Schuback, R., Travers, M., Vassiliev, H., Zimmer, A. and Zody, M., Direct, Submitted, Matthews, A. and Sody, M., Direct, Submitted, Matthews, A., Wallson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Schauer, A., A., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Schauer, A., A., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Schauer, A., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Schauer, S., Schuber, J., Viel, R., Wo, A., Wilson, M., Whitshead, Therithire, M., Wo, A., Wilson, Whitshead, Therithire, M., Wo, A., Wilson, Whitshead, Therithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wilson, Whitshead, Tharithire, M., Wo, A., Wilson, Whitshead, Tharithire, M., Wilson, Whitshead, Tharithire, M., Wang, M., Wilson, W
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All repeats were identified RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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HTG; HTGS PRASE1; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens (human)
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Cheege P. Describes J. Champopison, "Champopison," Champopison, Cheege P. Colangelo, M. Collinos F. Callymore A. Conk M. Cooke P. Describes J. Champopison, Chamber P. Fitthugh, M. Gage D. Galagan, J. Gardyna, S. Fritch, P. Fitthugh, M. Gage D. Galagan, J. Gardyna, S. Fritch, P. Fitthugh, M. Gage D. Galagan, J. Gardyna, S. Fritch, P. Fitthugh, M. Gage D. Galagan, J. Gardyna, S. Gardyna, S. Gardyna, S. Gardyna, S. Describ, M. Champarer, M. Johnson, R. Jonos, C. Hadoze, M. Gard, S. Garder, M. Garder, M. Garder, M. Garder, M. Garder, M. Garder, M. Garder, M. Garder, M. Garder, M. Matcham, K. Matcham, C. Garder, M. Jonos, C. Mander, M. Matcham, K. Matcham, C. Mander, M. Matcham, K. Matcham, C. Mander, J. Mander, M. Matcham, K. Matcham, C. Mander, M. Matcham, K. Matcham, C. Mander, J. Matcham, C. M. Garder, M. Matcham, K. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, C. Matcham, M. Sander, M. Sander, M. Sander, M. Schader, M. Sander, M. Sander, M. Schader, M. Sander, M. Sander, M. Sander, M. Matcham, M. Stolandry, M. Sander, M. Sander, M. Matcham, M. Stolandry, M. Wander, M. J. Matcham, M. Stolandry, M. Wander, M. J. Matcham, M. Matcham, M. Tander, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, C. Matcham, M. Matcham, C. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham, M. Matcham
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170057 ICTTATACACCAGCCCTCTTCTCTCTTTTTACACACCGCTTTGGCCATCACGTTCCAGTC 170116
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PN JP 2002112793-A/177
PD 16-APR-2002
PP 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE
PC C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K45/00, PC
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Haga, T.; Takeda, S. and Miyake, N.
Novel G-protein coupled receptors
Patent: JP 2002112793-A 177 16-APR-2002;
JAPAN Demokapiens (human)

PN JP 2002112793-A/177

PN JP 2002112793-A/177

PD 16-APR-2002

PD 09-FEB-2001 JP 2001034434

PT TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE
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                   ArgTyrAlaThrIleLeuThrAspThrIleIleAlaHisIleGlyValAlaAlaValVal
                                                                                        ArgGlySerLeuLeuMetLeuProCysProPhePheIleGlyArgLeuAsnPheCysGln
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                                                                                                                                                          SerHisValIleLeuHisThrTyrCysGluHisMetAlaValValLysLeuAlaCysGly
                                                                                                                                                                                                                          AspThrArgProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuValIleGlyValAsp
                                                                                                                                                                                                                                                                                            LeuPheCyslleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeuSerSer
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Novel G-protein coupled receptors
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Novel G-protein coupled receptors.
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JP 2002112793-A/177.
Homo sapiens (human)
Homo sapiens
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G01N33/566//
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CC Novel G-
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* is believed to be correct as given, however the sizes
• of the gaps between them are based on estimates that have
• provided by the submittor.
• This sequence will be replaced
• by the finished sequence as soon as it is available and
• the accession number will be preserved.
• 70427 70526: contig of 70426 bp in length
• 70527 78730: contig of 8204 bp in length
• 78731 78830: gap of 100 bp
• 78831 137440: contig of 58610 bp in length
• 137441 137540: gap of 100 bp
• 137541 203352: contig of 68812 bp in length.
Location/Qualifiers

b. 1. 203352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValCysGlyLeuGlyThrAlaThrIleValGlyAsnIleThrIleLeuValValValAla
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1. . 76426
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Matches:
Conservative:
Mismatches:
Indels:
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78831. 13744
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Query Match:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                  301 ValTyrGlyValLysThrLysGlnIleArgLysArgValValArgValPheGlnSerGly
       HislleHislleLeuLeuAlaAsnValTyrLeuLeuLeuProProAlaLeuAsnProVal
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                                                                                                                                                                      linear
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Novel proteins and nucleic acids encoding same
Patent: WO 0250276-A 35 27-JUN-2002;
Curagen Corporation (US)
Location/Qualifiers
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Mismatches:
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                                                                                                                                                                    AX551417 998 bp
Sequence 35 from Patent W00250276.
AX551417 GI:25814217
                                                                                                GlnGlyMetGlyIleLysAlaSerGlu 329
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 FEATURES
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TITLE Novel proteins and nucleic acids encoding same JODRNAL Patent: W0 0520776-A 37 27-JUN-2002; FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers About Targe="taxon:966" About Marches About	Oy 1 MetSerSerThrLeuGlyHisAsnMetGluSerProHisHisThrAspValAspProSer 20 2 4 TGTCCAGCACTCTTGGCCACAACTCCTAACTCTHTH	Oy 121 GluSerThrValLeuLeuAlaMetAlaPheAspArgTyrValAlaileCysHisProLeu 140 362 GAGTCCACTGGCCATGGCCTTGGTCGTGGCGATCGCCACCCCACT 141 ArgTyrAlaThrIleLeuThrAspThrIleIteAlaHisIleGlyValAlaAlaValVal 160 bb 422 CGCTATCCCCACATCGCCATCGCCATCGCCACATGGGGTGGCAGCTGTAGTG 481 cg cGCTATCCCCACATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTG 481 bb 422 CGCTATCCCCACATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTG 481 cg cGAGGCTCCCTGCTCATGCTCCCATCTTCTTGTGGCGTTTGAACTTCTGCCAA 541 bb 482 CGAGGCTCCCTGCTCATGTCCCTTCCTTATTGGGCGTTTGAACTTCTGCCAA 541 cg 3842 AGCCATGTGCTCCCATGTCCTTCTTTTTGGGCGTTTGAACTTCTGCCAA 541 cg 3842 AGCCATGTGATCCTTATTGGGCGTTTGAACTTCTGCCAA 541 cg 3842 AGCCATGTGATCCTTATTGGGCGTTTGAACTTCTGCCAA 541 cg 3842 AGCCATGTCACACACGTAGTGAGCACTTGGTGGAGCTGTGGGA 601 cg 3842 AGCCATGTCACACACGTAGTTGAGCACTTGGTGAAGCTGGCCTTTGGAG 601 cg 3842 AGCCATGTCACACACACATGTCATTGAGCTGTTGGAGCTGGCCTTTGGAG 601
61 ThrGlubroValleuHisly8ProValTyrLeuPheLeuCy8MetLeuSerThrIleAsp 80 182 ACTGAACCAGTCTTGCACAGCCTGTGTACTTTTTTGTGTCTCTCTAACCATGAC 241 81 LeuAlaAlaSerValSerThrValProLysLeuLeuAlaIlePheTrpCysGlyAlaGly 100 242 TTGGCTGCTCTGTCTCCACAGTTCCTAACCATCTTCTGGTGTGGAGCCGGA 301 101 HisleSerAlaSerAlaCy8LeuAlaHisMetPhePheIleHisAlaPheCy8MetMet 120 112 GluSerThrValLeuLeuAlaMetAlaPheAspArGTTCTTCATTCATGCTGTGCAGGCGGAGCGGAGGGAGCGATGTCTTCATTCA	221 LeupheCyslleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeuSerSer 240 662 TTGTTTTGCATTGCATTGCCTTAGCCTTAGCTGTCCTTCGCTTCTCTCTTCTTCTTCTTCTTCTTCTTC	AX551419 MX551419 Sequence 37 from Patent W0025076. ESSION AX551419.1 GI:25814219 SION AX551419.1 GI:25814219 SION AX551419.1 GI:25814219 Homo sapiens (human) RCE Homo sapiens (human) RCE Homo sapiens (hordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo. ELNENCE Li,L., Padigaru,M., Ballinger,R.A., Kekuda,R., Colman,S.D., Sciore,P., Smithson,G., Peyman,J.A., Macdougall,J.R., Stone,D., Vernet,C.A., Shenoy,S., Gunther,E., Millet,I., Tcherney,V.T., Anderson,D., Gusev,V., Malyankar,U.M., Zhong,H., Ellerman,K.E. and Wolenc,A.

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AB065534 1390 bp DNA linear PRI 23-JUL-2002
Homo sapiens gene for seven transmembrane helix receptor, complete
                                       GICTICITICITICICICGGGCATCCCAGGTCTGGAACAATTTCATTTGTGGCTCTCACTCCCT
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Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 797 02-JAN-2003;
Mational Institute of Advanced Industrial Science and Technology
(JP); Center for Advanced Science and Technology (JP)
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                                                               722 CATGAAGCTCGGTCCAAGGCCCTAGGGACCTGGTTCCCATGTCTGTGTTCTATCCTCATC
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SerTyrThrProAlaLeuPheSerPhePheThrHisArgPheGlyHisHisValProVal
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Homo sapiens chromosome 11 clone RP11-658K18, WORKING DRAFT SEQUENCE, 19 unordered pieces.
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Waterston,R.H.
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                                                                                        381 ACTGAACCAGTCTTGCACAAGCCTGTGTACCTTTTTTCTGTGCATGCTCTCAACCATCGAC
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                                                   ThrGluProValLeuHisLysProValTyrLeuPheLeuCysMetLeuSerThrIleAsp
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
Submitted (CBRC), National Institute of Advanced Industrial Science
Center (CBRC), National Institute of Advanced 135-0064, Japan
and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
(B-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
Tel:81-3-3599-8080, Fax:81-3-3599-8081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              our automated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding (Genebecoder), sequence search, motif-domain assignment and transmembrane helix prediction.

And the sequence is submitted by the collaborative project between (Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST) and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                           Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S., Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y. Genome-wide discovery and analysis of human seven transmembrane
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Matches:
Conservative:
Mismatches:
Indels:
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                 isolate:CBRC7TM_97
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AB065534.1 GI:21928364
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Unpublished
                                                                                                               Homo sapiens (human)
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                                                                                                                                          Homo sapiens
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Best Local Similarity:
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REFERENCE
AUTHORS
TITLE
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                                              ACCESSION
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KEYWORDS
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61 ThrGluProValLeuHisLysProValTyrLeuPheLeuCysMetLeuSerThrlleAsp 80
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Matches:
Conservative:
Mismatches:
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147719. .171498
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171599. .172027
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100120. .114785
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        172027: contig of 429 bp
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/organism="Homo sapiens"
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/~rymon_come="11"
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                       Location/Qualifiers
1. .172027
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                                                                         St. Louis,
                                           Submitted (19-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MN 63108, USA On Sep 1, 2000 this semisors
                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                 63108, USA
Sep 1, 2000 this sequence version replaced gi:9838305
                                                                                                                                                               Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s: contig of 1526 bp in length
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s: contig of 11102 bp in length
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s: gap of unknown length
s: contig of 9895 bp in length
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g of 15622 bp in length
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of 14666 bp in length
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              2 (bases 1 to 172027)
Waterston, R.H.
Direct Submission
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Submitted (15-MR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

18 J [bases 1 to 176597]

8 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N. Bastlen, V., Bloom, T., Boguslavkiy, L., Chargollo, M., Campoplano, A., Chang, J., Campoplano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gande, S., Gorder, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Ilev, I., Glangello, R., Jones, R., Jones, C., Macdenald, P., Mals, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLen, C., Macdenald, P., Malori, J., Marquis, N., Matthews, C., McCarthy, M., McRwan, P., McKernan, K., Maldrim, J., Meneus, L., Nihora, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., O'Connor, T., O'Connell, P., Pierre, N., Fale, C., Rogov, P., Roman, C.H., O'Connor, T., O'Connell, P., Pierre, N., Schupback, R., Schauer, S., Schupback, R., Senace, R., Schauer, S., Schupback, Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Y., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., Wills, N., Yoo, A., and Zody, M.

Direct Submission
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclan, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McFernan, K., Melladin, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Rieback, M., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J. Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainou, J., Zambek, L., Zimmer, A. and Zody, M., Vann, Conter for Ganner, C., L., Zimmer, A., Lander, A., Talan, A., Talan, A., Talan, A., Talan, A., Talan, A., Talan, A., Ye, W.J., Young, G., Sainou, J., Ye, W.J., Young, G., Sainou, J., Ye, W.J., Young, G., Sainou, J., Ye, W.J., Young, G., Sainou, J., Ye, W.J., Young, G., Sainou, J., Karliev, R., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, S., Sainer, S., Shore, J., Willer, R., Schoup, G., Calinds, G., Sainer, J., Wasiliev, H., Vola, W., Waller, M., Wayan, D., Ye, W.J., Young, G., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sainer, A., Sai
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Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 176597)
B birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Roukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A.,
Ginde, S., Gorde, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
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Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Ianders, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLen, C., Morman, C. H., O'Connor, J., Marquis, N., Matthews, C.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Oliver, J., Peterson, K., Phunkhang, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., O'Neil, D.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Yoham, K., Travers, M., Travis, M., Triglilo, J., Vassillav, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 176597)
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Homo sapiens chromosome 11, clone RP11-44D14, complete sequence.
AC116156
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
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                                                                                                                                                                                                                                                                                                                   HislleSerAlaSerAlaCysLeuAlaHisMetPhePheIleHisAlaPheCysMetMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluSerThrValLeuLeuAlaMetAlaPheAspArgTyrValAlaIleCysHisProLeu
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Submitted (10-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA AUTHORS It to 176597) Birren,B. Linton,L. Nusbaum,C., Lander,E., Ali,A., Allen,N., Bartien,B., Choepel,Y., Colangelo,M., Callins,S., Collymore,A., Coke,P., DeArellano,M., Collins,S., Collymore,A., Cook,A., Cook,P., DeArellano,M., Dast, M., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Cardyas,S., Govette,M., Grade,B., Garade,B., Gord,S., Govette,M., Grade,R., Candarare,R., Lamazares,R., Landers,H., Lehore,K., Lamazares,R., Landers,A., Karates,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Mancon,T., Monso,C., Macdonald,P., Major,J., Matthews,C., Macdonald,P., Major,J., Matthews,C., Micol,R., Maylor,J., Matthews,C., Micol,R., Maylor,J., Maylor,J., Micol,R., Micoland,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Raymond,C., Rette,R., Rieback,M., Rise,C., Rogdov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Stange-Thomann,N., Stojanovic,N., Stranss,M., Travis,N., Traigilio,J., Vassiliev,H., Viel,R., Vola,R., Wiel,R., K., Wiel,R., K., Wiel,R., K., Wiel,R., K., Wiel,R., Wiel,	TITLE CALIDOLIO., 2 Cambek, L., ZIMMer, A. and Zody, M. Direct Submission Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA COMMENT On May 10, 2002 this sequence version replaced gi:20177753. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center: code: WIBR Web site: http://www.seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project name: 126176 Center zone name: 44_D_14	FEATURES Location/Qualifiers 1176597 / organism="Homo sapiens" / organism="Homo sapiens" / db xref="teaxon:9606" / chromosome="11" / map="11" / clone="RP11-44D14" /	

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Oy 121 GluSerThrValLeuLeuAlaMetAlaPheAspArgTyrValAlaIleCysHisProLeu 140	Qy 181 SerHisVall1eLeuHisThrTyrCyBGluHisMetAlaValValLysLeuAlaCySGly 200 Db 158729 AGCCATGTGATCCTACACGTACTGAGGCACATGGCTGTGGTGATGGCTGTGGTGAG 158670 Qy 201 ASpThrArgProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuVallleGlyValAsp Db 158669 GACACCAGGCCTAACGTGTGATGGCTGACAGCTGCACATTGGGGTTGAC	2 4 6 4	Qy 261 SerTyrThrProAlaLeuPheSerPhePheThrHisArgPheGlyHisHisValProVal 280 Db 158489 TCTTATACACCACCTCTTCTCTTTTTACACCACTTTTGCCATCACGTTCACGTC 158430 Qy 281 HisTleLeuLeuAlaAsnValTyrLeuLeuLeuLeuProProAlateuAsnProVal 300 Db 158429 CATATTCACATTTTTGGCCAATGTTTTGCCACTGTTTTTGCCACTGTTTACTGTT	Qy 301 ValTyrGlyValLysThrLysGln1leArgLysArgValValArgValPheGlnSerGly 320 Db 158369 GTATATGGAGTTAAAGACCAAACAGATCCGTAAAAGAGTTGTCAGGGTTTTCAAAGTGGG 158310 Qy 321 GlnGlyMetGlylleLysAlaSerGlu 329 Db 158309 CAGGGAATGGCCATCAAGGCATCTGG 15823	SULT 10 241675 A CUS A CUS A CESSION A RSION A TWORDS A	NISM NCE ORS	TITLE OIRCOTY RECEPTOR SEQUENCES JOURNAL PATENT: WO 0127158-A 423 19-APR-2001; JOURNAL PATENT: WO 0127158-A 423 19-APR-2001; FEATURES Location/Qualifiers Location/Qualifiers 1. 963	ORIGIN Alignment Scores: Alignment Scores: Pred. No.: Score: Score: Percent Similarity: 99.07\$ Mismatches: Best Local Similarity: 98.75\$ Mismatches: 3

Db 541 TOTOAGCACATGGGTGAAGCTGGCAGACACCAGGGCTAACCGTGTAACGGTGTAACGGTGTAACGGTGTAACGGTGTAACGGTGAA	Alignment Scores: 1.27e-147 Length: 966 Score: 1649.00 Matches: 317 Percent Similarity: 99.07% Conservative: 1 Best Local Similarity: 98.75% Mismatches: 3 Query Match: 6 Gaps: 0	
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Birren, B. Lininon, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, M., Bastison, V., Boudslatkiy, L., Boukhgaiter, B., Brown, A., Camara, J., Campopiano, A., Chang, J., Chazaro, B., Chocka, Cooke, P., DeArellano, K., Dearino, C., Chang, J., Chazaro, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Gnode, S., Gord, S., Goyette, M., Garel, D., Galagan, J., Gadayna, S., Grafas, S., Gord, S., Goyette, M., Garel, D., Galagan, J., Gadayna, S., Grafas, P., Frizhugh, W., Gage, D., Galagan, J., Gadayna, S., Gandes, S., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Hagos, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Marden, C., Marchan, K., Margia, M., Matlewa, C., Micchi, C., Morman, C. H., O'Connor, T., Orbonnell, P., O'Neil, D., Oliver, J., Norman, C. H., O'Connor, T., Naylor, J., Nouven, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., Naylor, J., Nouven, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., Naylor, J., Nouven, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., Naylor, J., Nouven, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T. O'Connor, T.,
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                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 202761)
sapiens chromosome 11, clone CTD-2504M7, complete sequence
                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone CTD-2504M7 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProLysLeuLeuAlaIlePheTrpCysGlyAlaGlyHisIleSerAlaSerAlaCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 GCCTTTGATCGCTACGTGGCCATCTGCCACCCCACTCCGCTATGCCACACTCCTCACTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysGluHisMetAlaValValLysLeuAlaCysGlyAspThrArgProAsnArgValTyr
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                                                                MetGluSerProHisHisThrAspValAspProSerValPhePheLeuLeuGlyIlePro
                                                                                                                       1 Anggaarcrecraarcaeaergargrigaeeerrergrerrerrerreereerggeareea
                                                                                                                                                                                  29 GlyLeuGluGlnPheHisLeuTrpLeuSerLeuProValCysGlyLeuGlyThrAlaThr
                                                                                                                                                                                                                                                                                                   IleValGlyAsnIleThrIleLeuValValValAlaThrGluProValLeuHisLysPro
                                                                                                                                                                                                                                                                                                                                           121 ATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTGAACCAGTCTTGCACAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                     ValTyrLeuPheLeuCysMetLeuSerThrIleAspLeuAlaAlaSerValSerThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyLeuThrAlaAlaLeuLeuValIleGlyValAspLeuPheCysIleGlyLeuSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 GGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTTGCATTGGTCTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 GCCCTAAGTGCACAAGCTGTCCTTCGCTCTCATCCCATGAAGCTCGGTCCAAGGCCCTA
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Matches:
Conservative:
Mismatches:
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complement (13.044. .1343)

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complement(30926. 30987)
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1647.50
98.18%
98.18%
95.90%
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28928.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T. Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., McEwan, P., McGarran, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retersen, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schubback, R., Seman, S., Severy, P., Spencer, B., Stange, Thoman, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wayan, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Ye, W. J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                             Submitted (14-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street. Cambridge, MA 02141, USA On MAY 44, 2002 this sequence version replaced gi:20429487.

All repeats were identified using RepeatMasker:
Smir, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L24591
Center clone name: 2504_M_7
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1 MetSerSerThrLeuGlyHisAsnMetGluSerProHisHisThrAspValAspProSer 20
Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J. R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E. H., Masiello, C., Makkeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

The accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-DEC-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180937 bases at least 040
Consensus quality: 181081 bases at least 030
Consensus quality: 181163 bases at least 020
Insert size: 177000; agarose-fp
Insert size: 181386; sum-of-contigs
Quality coverage: 12.99x in Q20 bases; sum-of-contigs
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/clone lib="CH256"
/note="BAC resource: http://bacpac.chori.org/"
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Center code: NISC
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/mol type="genomic DNA"
/db_xref="taxon:30611"
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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Center clone name: 553F22
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vector_side:right"
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Otolemur garnettii clone CH256-553F22, WORKING DRAFT SEQUENCE.
AC147586.
AC147586.
AC147586.1 GI:40018680
HTG5.PHASE2; HTGS_DRAFT.
Otolemur garnettii (small-eared galago)
Otolemur garnettii (small-eared galago)
Otolemur garnettii (small-eared galago)
ADMARAYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
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                                                                      aThrGlubroValLeuHisLysProValTyrLeuPheleuCysMetLeuSerThrIleAs
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  ValPhePheLeuLeuGlyIleProGlyLeuGluGlnPheHisLeuTrpLeuSerLeuPro 40
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AC146635 Otolemur garnettii clone CH256-105A13, WORKING DRAFT SEQUENCE, 4

AC146635

AC146635/c DEFINITION ACCESSION KEYWORDS VERSION

ordered pieces. AC146635 AC146635.2 GI:37700288 HTG; HTGS_PHASE2; HTGS_DRAFT.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.

1. (Dases 1 to 23935)

2. Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,B.,
Coleman,H., Benje,J., Granite,S., Gunta,J., Haghighi,P., Han,J., Hansen,N., Han,S.-L., Hu,P., Hurle,B., Idol,J.R.,
Karlins,E., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
Legaspi,R., Maduro,O.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
Maskeri,B., McDowell,J., Mullikin,J.C., Paguirigan,C., Pearson,R.,
Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W.,
Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-007-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Oct 17, 2003 this sequence version replaced gi:34576313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center, 8717
77, USA
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Sequencing vector: plasmid; n/a: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 238379 bases at least Q40
Consensus quality: 238629 bases at least Q20
Consensus quality: 238629 bases at least Q20
Insert size: 239035; sum-of-contigs
Quality coverage: 10.78x in Q20 bases; sum-of-contigs
Quality coverage: 10.78x in Q20 bases; sum-of-contigs
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

4357: contig of 4357 bp in length

4458 4457: gap of unknown length
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Center code: NISC
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Grovemont Circle, Gaithersburg, MD 20877,
3 (bases 1 to 239335)
       garnettii (small-eared galago)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: nisc_zoo@nhgri.nih.gov
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                                    Otolemur garnettii
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                                       ORGANISM
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AGCCACGTGATCCTGCACATACTGTGAGCACATGGCGGTTGTGAAGCTGGCCTGTGGA
                                                                                                                                                LeuPheCysIleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeuSerSer
                                                               201 AspThrArgProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuValIleGlyValAsp
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        4458 66663; contig of 62206 bp in length 6664 26763; gap of unknown length 6764 232439; contig of 165676 bp in length 2540 232539; gap of unknown length 2540 239335; contig of 6796 bp in length. Location/Qualifiers 1. 239335 /organism="">Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Loca
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' Search time 548 Seconds
(without alignments)
2954.652 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                          OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                              August 27, 2004, 18:39:29
```

Run on:

US-10-081-775-2 1718 1 MSSTLGHNMESPHHTDVDPS......RKRVVRVFQSGQGMGIKASE 329 3237270 segs, 2460713050 residues 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Perfect score: Scoring table: Searched: Sequence:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USTPTO spool/USIO081775/runat_20082004_170214_11184/app_query.fasta_1.519
-Q=/cgn2_1/USTPTO spool/USID081775/runat_20082004_170214_11184/app_query.fasta_1.519
-DB=Published Applications NA -QFMT=fastap -SUFFIX=nnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRART=1 -END=-1 -MATRIX=blosun62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MN=0 -ALIGN=15 -MODEL-LOCAL -OUTFMT=pto -NORM=axt -HRAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=USI008175_@CGN 1 1 480 @runat_20082104_170214_11184
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NGS_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG -DEV_TIMEUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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"(cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*)" Published_Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB

Description

Sequence 1, Appli	ď	Sequence 262	e 353	e 35. p	equence 37,	equence 92	equence 797.	42.	a:	959	Sequence 315, App	157		e 945,	819.	23.	16	114.	Sequence 114.	equence 213,	equence 15.	equence 31.	equence 909.	equence 783	equence 17.	equence 25,	Sequence 947, App	821	102,	10	19	equence 1,	edneuce 81	equence 3,	equence 21	Sequence 29,	Seguence 260, App	e 260	equence 185	equence 91.	equence 92	equence 799	equence 159	equence 19.	
US-10-0	09-886-055-26	US-09-804-291-26	US-10-343-650A-353	US-10-025-806-35	US-10-025-806-3	-10-017-161	US-10-292-798-79	US-10-297-0	US-10-292-798-83	US-10-017-161-95	US-10-343-	US-10-387-629-157	US-10-467-25	US-10-017-161-94	US-10-292-798-8	US-10-182-822A-2	US-10-044-643-19	-886-055-11	US-09-804-291-1	US-10-343-650A-	US-10-044-643-15	US-10-220-382-3	US-10-017-161-90	US-10-292-798-7	US-10-044-643-1	US-10-025	US-10-017-161-9	US-10-292	US-09-886-	US-09-804	US-10-343-650A-1	US-10-025-806-1	US-10-017	US-10-025-806-3	US-09-844-861A	US-10-466-720-2	09-886-055-26	9-804-2	US-10-343-650A-189	-10-024-212-9	US-10-017-161-925	-10-292-798-79	-10-343-6	1A-1	
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR, HGPREMY25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES
FILE REFERENCE: D0126 NP 1026 NP 1 Sequence 1, Application US/10081775 Publication No. US20030060409A1 GENERAL INFORMATION: TYPE: DNA ORGANISM: homo sapiens RESULT 1 US-10-081-775-1

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ArgTyrAlaThrIleLeuThrAspThrIleIleAlaHiBileGlyValAlaAlaValVal 160
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            1437 GTATATGGAGTTAAGACCAAACAGATCCGTAAAGAGTTGTTGAGGTGTTTCAAAGTGGG 1496
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ValTyrGlyValLysThrLysGlnIleArgLysArgValValArgValPheGlnSerGly
                                                                                                                                                                                PERCEPTION, AND
                                                                                                                 Sequence 222, Application US/09886055
; Sequence 222, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
    APPLICANT: STYER, UJUERT
    APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERC
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT FILING DATE: 2000-6-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR APPLICATION NUMBER: 60/213,812
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PATENTIN VOX: 2.1
; SEQ ID NOS: 522
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Conservative:
Mismatches:
Indels:
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CORGANISM: Homo sapiens
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Percent Similarity:
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Matches:
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       ; LOCATION: (537)..(1523)
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1691.00 Matches: 325	4. Valcy861y16u01y1hrAlaThrIleVal01yAsmileThrIleLeuValValAla 60	HisileSerAlaSerAlaCysLeuAlaHisMetPhePheIleHisAlaPheCysMetMet 1	ArgGlySerLeuLeuMetLeuProCysProPhePheIleGlyArgLeuAsnE	GACACCAGGCCTAACCGTGTGTATGGGCTGACAGCTGCTGTTGGTCATTGGGGGTTGAC LeuPheCys1leGlyLeuSerTyrAlaLeu1leAlaGlnAlaValLeuArgLeuSerSer	721 CATGAAGCTCGGTCCAAGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATC 780 261 SerTyrThrProAlaLeuPheSerPhePheThrHi8ArgPheGlyHi8Hi8ValProVal 280	281 HislleHislleLeuLeuAlaAsnValTyrLeuLeuLeuLeuLeuLeuAsnBroVal 300 	301 ValTyrGlyValLysThrLysGlnIleArgLysArgValValArgValPheGlnSerGly 320
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HislleHislleLeuLeuAlaAsnValTyrLeuLeuLeuProProAlaLeuAsnProVal 300
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                             541 AGCCATGTGATCCTACACACGTACTGTGAGCACATGGCTGTGGTGAGCTGGCCGTGTGGG
                                                                AspThrArgProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuValIleGlyValAsp
        SerHisValileLeuHisThrTyrCysGluHisMetAlaValValLysLeuAlaCysGly
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APPLICANT: Gusev, Vladinir
APPLICANT: Malyankar, Uriel
APPLICANT: Zhong, Haihong
APPLICANT: Ellerman, Karen
APPLICANT: Nolenc, Acaren
APPLICANT: Nolenc, NoveL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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CURRENT APPLICATION NUMBER: US/10/025,
CURRENT FILING DATE: 2001-12-19
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PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/259,743
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/299,327
PRIOR FILING DATE: 2001-06-19
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; Sequence 35. Application US/10025806
; Publication No. US20030198955A1
; GENERAL INFORMATION:
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Milet, Isabelle
Tchernev, Velizar
Anderson, David
Gusev, Vladimir
Malyankar, Uriel
Zhong, Haihong
Ellerman, Karen
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Peyman, John
MacDougall, John
Stone, David
Vernet, Corine
Shenoy, Suresh
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Casman, Stacie
Edinger, Shlomit
Gerlach, Valerie
Sciore, Paul
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                                                                                                                     TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR PILING DATE: 2000-08-04
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
NUMBER: OF SEQ ID NOS: 694
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 353
LENGTH: 990
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961 CAGGGAATGGGCATCAAGGCATCTGAG 987
                                                                        ; Sequence 353, Application US/10343650A; Publication No. US20040067499A1; GENERAL INFORMATION:
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Query Match:
DB:
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US-10-343-650A-353
                                                             -10-343-650A-353
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Pred. No.:
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                                                  ArgGlySerLeuLeuMetLeuProCysProPhePheIleGlyArgLeuAsnPheCysGln
                                                                         CAAGGCTCCCTGCTCATGCTCCCATGTCCCTTATTGGGCGTTTGAACTTCTGCCAA
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APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: Zhong, Haihong
APPLICANT: Elleman, Karen
APPLICANT: Bleam, Karen
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOWEL PROTEINS AND CURRENT APPLICATION NUMBER: US/10/025, 806
CURRENT APPLICATION NUMBER: US/10/12-19
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GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rekuda, Rameeh
APPLICANT: Colman, Steven
APPLICANT: Colman, Steven
APPLICANT: Genan, Steven
APPLICANT: Genan, Stacie
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APPLICANT: Smitheon, Glennda
APPLICANT: Smitheon, Glennda
APPLICANT: Stone, David
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PRIOR APPLICATION NUMBER: 60/256,635
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: 60/261,498
PRIOR FILING DATE: 2001-01-2
PRIOR PLILNG DATE: 2001-01-24
PRIOR PLILNG DATE: 2001-01-24
PRIOR PLILNG DATE: 2001-02-24
PRIOR PLICATION NUMBER: 60/276,464
PRIOR APPLICATION NUMBER: 60/271,021
PRIOR APPLICATION NUMBER: 60/275,946
PRIOR PILING DATE: 2001-02-22
PRIOR PLING DATE: 2001-03-24
PRIOR PLILNG DATE: 2001-03-14
PRIOR PLILNG DATE: 2001-03-14
PRIOR PLILNG DATE: 2001-03-23
PRIOR PLILNG DATE: 2001-03-23
PRIOR FILING DATE: 2001-04-23
PRIOR PLILNG DATE: 2001-08-16
PRIOR PLILNG DATE: 2001-08-16
PRIOR PLILNG DATE: 2001-08-16
PRIOR PLILNG DATE: 2001-08-16
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 352
SOFTWARRE: PATENTIN VET: 2.1
SEQ ID NO 35
FLENGTH: 998
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1691.00
99.09%
98.78%
98.43%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (2)
US-10-025-806-35
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Pred. No.:
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ValTyrGlyValLysThrLysGlnIleArgLysArgValValArgValPheGlnSerGly 320
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482 caaddciccidcicaldciccatdicciliccilatidadacticidaa
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                                                             141 ArgTyrAlaThrIleLeuThrAspThrIleIleAlaHisIleGlyValAlaAlaValVal
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Publication No. US20030143668A1

GENERAL INFORMATION

APPLICANT: SUWA, MAKIKO

APPLICANT: SUWA, YUTAKA

APPLICANT: AKIYAMA, YUTAKA

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT FILING DATE: 2002-12-18

FRIOR APPLICATION NUMBER: UP 2001/246789

PRIOR PILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE PATENTIN VOYE: 2.1
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; LOCATION: (201)..(1166)
US-10-017-161-923
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ORGANISM: Homo sapiens
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LOCATION: (1)..(
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      PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/259,743
PRIOR APPLICATION NUMBER: 60/299,327
PRIOR APPLICATION NUMBER: 60/299,327
PRIOR PILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-2
PRIOR PRIOR PAPLICATION NUMBER: 60/264,664
PRIOR APPLICATION NUMBER: 60/276,464
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-13
PRIOR PRILING DATE: 2001-03-13
PRIOR PRILING DATE: 2001-03-13
PRIOR PRILING DATE: 2001-03-15
PRIOR PRILING DATE: 2001-03-16
PRIOR PRILING DATE: 2001-03-16
PRIOR PRILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
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US-10-025-806-37
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DS-10-222-/98-/97, Application US/10292798

Publication No. US2003023833A1

GENERAL INFORMATION:

APPLICANT: SUNA, MAXINO

APPLICANT: ARIYAMA, VURKA

APPLICANT: ARIYAMA, VURKA

APPLICANT: ARIYAMA, VURKA

APPLICANT: ARIYAMA, VURKA

TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

TITLE OF INVENTION UNMERR: US/10/292,798

CURRENT PILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US/2012-11-13

PRIOR APPLICATION NUMBER: UP 2001-246789

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SEQ ID NO 797

LENGTH: 1390

MAYOR: NASE APPLICATION VOR 12-16

SEQ ID NO 797

LENGTH: 1390
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; LOCATION: (201)..(1190)
US-10-292-798-797
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)..(1390)
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                     US-10-292-798-797
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Mismatches:
Indels:
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Matches:
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                                  Percent Similarity:
Best Local Similarity:
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APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, HIROYUKI
ITILE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152 uS/10/017,161
CURRENT APPLICATION NUMBER: US/10/017,161
FRIOR APPLICATION NUMBER: UP 2001/246789
FRIOR APPLICATION NUMBER: UP 2001/246789
FRIOR APPLICATION NUMBER: UP 2001/246789
FRIOR APPLICATION NUMBER: 202-12-18
FRIOR APPLICATION NUMBER: UP 2001/246789
FRIOR FILING DATE: 2001-06-18
FRIOR FILING DATE: 2001-06-18
FRIOR FILING DATE: 2101-06-18
FRIOR FILING DATE: 2101-06-18
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Publication No. US20030143668A1
GENERAL INFORMATION:
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; FRATURE:
; NAME/KEY: CDS
; LOCATION: (526)..(1042)
US-10-017-161-959
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ORGANISM: Homo sapiens
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NAME/KEY: BOURCE
LOCATION: (1)..(1242)
FEATURE:
NAME/KEY: CDS
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Pred. No.:
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                                                                                                                                                    Sequence 833, Application US/10292798

Publication No. US2003023833A1

GENERAL INFORMATION:

APPLICANT: SUWA, MAKINO

APPLICANT: ASAI, KIYOSHI

APPLICANT: ASAI, KIYOSHI

APPLICANT: ARIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 044335/166

CURRENT PAPLICATION NUMBER: US/10/292,798

CURRENT FILING DATE: 2001-12-18

FRIOR APPLICATION NUMBER: US/201-246789

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 833

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                                                 US-10-081-775-2 (1-329)
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US-10-343-650A-315
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                                                APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUFLED REC
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR APPLICATION NUMBER: JP 2001/34434
SOFTWARE OF SEQ ID NOS: 694
SOFTWARE: Patentin Ver: 2.1
LENGTH: 990
Sequence 315, Application US/10343650A Publication No. US20040067499A1 GENERAL INFORMATION:
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931.50
73.91%
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US-10-343-650A-315
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LOCATION: (1)
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; Publication No. US20040115676A1
; GENERAL INFORMATION:
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US-10-467-252-93
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Publication No US20030221205A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Veithen, Alex
TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
FILE REPERENCE: 9409/2192
CURRENT APPLICATION NUMBER: US/10/387,629
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 254
SOFTWARE: Patentin version 3.1
SEQ ID NO 157
LENGTH: 990
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ORGANISM: Homo Sapiens
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US-10-387-629-157
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Best Local Similarity:
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US-10-387-629-157
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763 CCAGGGAGTGAGGCCCGACTTAAGGCGTTTAGCACATGTGGCTCTCATATTTGTGTCATC
                                             LeulleSerTyrThrProAlaLeuPheSerPhePheThrHisArgPheGlyHisHisVal
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APPLICANT: ASAI KIYOSHI
APPLICANT: ASAI KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ARINAMA, YUTAKA
APPLICANT: ARBURATAN, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPRENCE: 084335/0152
CURRENT FELLING DATE: 2002-12-18
PRIOR FILING DATE: 2002-12-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PAGENTIN VEY: 2.1
SEQ ID NO 945
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Matches:
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; OTHER INFORMATION: a, t,
US-10-017-161-945
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LOCATION: (201)..(1190)
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NAME/KEY: SOURCE
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FEATURE:
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Best Local Similarity:
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; OTHER INFORMATION: Incyte ID No: 7475226CB1
US-10-467-252-93
      PRIOR APPLICATION NUMBER: US 60/280,597
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/281,107
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 93
LENGTH: 1114
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                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: 2hou, Ping
APPLICANT: 2hou, Ping
APPLICANT: Asunda, Vinod
APPLICANT: Asunda, Vinod
APPLICANT: Andray Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-09-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PL_Genes Version 2.0
SEG IN NO 13
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US-09-016-414-1312
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US-09-016-414-1104
US-09-016-414-1105
US-09-016-414-1363
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Tang, Y. Tom
Liu, Chenghua
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/Cqn2_1/USPTO spool/US10081775/runat_20082004_170214_11153/app_query.fasta_1.519
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NG NMAP -LARGEQUERY -NGG SCORES=0 -MAIT -DSPELOCK=100 -LONGLOG
-PEV_TIMBOUT=120 -WARN_TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                            OM protein - nucleic search, using frame_plus_p2n model
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US-09-439-313-526
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US-09-685-166A-526
US-08-465-980-1
US-09-053-303-1
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Xu, Jiangchun
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                                                                                                                                                                                               LeuAlaMetAlaPheAspArgTyrValAlaIleCysHisProLeuArgTyrAlaThrIle 145
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                                                                                                        697 CTTGTAGCACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTT 756
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                                                                                       GlylleProGlyLeuGluGlnPheHisLeuTrpLeuSerLeuProValCysGlyLeuGly 45
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Mismatches:
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 Matches:
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69.70%
52.53%
50.49%
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Sequence 526, Application US/09439313 Patent No. 6329505 GENERAL INFORMATION:

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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Renger, Gary
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Boly, Crabo
INVENTION: COMPOSITIONS AND METHODS FOR THER
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.42709
FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION S. 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
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CRGANISM: Homo sapiens
US-09-439-313-526
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                                                                   80 AspLeuAlaAlaSerValSerThrValProLysLeuLeuAlaIlePheTrpCysGlyAla
                          .45 AGGACGGAACCCACCCCCACATGTACCTCTTTCTCTGCAGCTTGCAGCCATT
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; Patent No. 6630305
; GENERAL INFORMATION:
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susian L.
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AspleuPheCysIleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeuSer 239
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 963
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Patent No. 6620922
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Ranger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapiens
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Best Local Similarity:
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TYPE: nucleic acid
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                                AND
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY JITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5.26
LENGTH: 963
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US-09-685-166A-526
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260 IleSerTyrThrProAlaLeuPheSerPhePheThrHisArgPheGlyHisHisValPro 279
                                                                                                                                        ValvalTyrGlyValLysThrLysGln1leArgLysArgValValArgValPheGln 318
                                                                                                                                                                                                                                            APPLICANT: Soppet, Daniel R. APPLICANT: L1, Yi APPLICANT: Rosen, Craig A. APPLICANT: Rosen, Craig A. APPLICANT: Rosen, Steven M. TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70 NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STREET: 6 BECKER FARM & OLGTEIN STREET: 6 BECKER FARM Road CITY: Roseland
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: PETRATO GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 325800-446
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TELEFRANCE/DOCKET NUMBER: 325800-446
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Mismatches:
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Matches:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET UNBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1474 base pairs
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856.00
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1:
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; LOCATION:
US-09-053-303-1
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           COUNTRY:
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44 LeuGlyThrAlaThrIleValGlyAsnIleThrIleLeuValValValAlaThrGluPro
                                                               64 ValLeuHisLysProValTyrLeuPheLeuCysMetLeuSerThrlleAspLeuAlaAla
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APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09053303
Patent No. 5948890
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CITY: Roseland
STATE: New Jerse
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1474
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Length:
Matches:
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                                                                                     ProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuValIleGlyValAspLeuPheCys 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09/339.115
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,303
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09339115
Patent No. 6372891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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284 IleLeuLeuAlaAsnValTyrLeuLeuLeuProProAlaLeuAsnProValValTyrGly 303
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48
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Matches:
Conservative:
Mismatches:
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856.00
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54.24%
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CDNA
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Query Match:
MOLECULE TYPE:
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Best Local Similari
                                                                                                                   Alignment Scores:
                                    NAME/KEY:
; LOCATION:
US-09-339-115-1
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1090 GTTGTCATGGGTGACATCTACCTGCTGCTGCTGTCATCAATCCCATCATCTATGGT 1149
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                  430 AGCCTGCACGCTCCGATGTACCTCTTTCTCTGCATGCTTGCAGCCATTGACCTGGCCTTA 489
                                                                                                                                                                      104 AlaSerAlaCysLeuAlaHisMetPhePheIleHisAlaPheCysMetMetGluSerThr 123
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                                                                                                      204 ProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuValIleGlyValAspLeuPheCys
                                                                     SerValSerThrValProLysLeuLeuAlaIlePheTrpCysGlyAlaGlyHisIleSer
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
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; Sequence 5, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
    APPLICANT: Ronnett et al.
    TILLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                  304 ValLysThrLysGlnIleArgLysArgValValArgValPheGln 318
                                                                                                                                                                                              APPLICANT: Soppet, Daniel R.
APPLICANT: Soppet, Daniel R.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRE
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APPLICATION NUMBER: PCT/US95/07093
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                      RESULT 8
PCT-US95-07093-1
| Sequence 1, Application PC/TUS9507093
| GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Floppy disk
IBM PC compatible
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                           6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.24e-91
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy
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: USA
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Query Match:
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TELEFAX: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US95-07093-1
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127 GTATCACTAACAGGAATACTCTCATAGCCCTTGCTATTTGTACCAGTCCATCTCTACAC 186
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790 ACCTATTGAGGCCCAAGTCTAGCCAC----TCACCAGGAATGGACAAATTCTTGGCC 843
                                                                        288 AsnVallyrLeuLeuLeuProProAlaLeuAsnProValValTyrGlyValLysThrLys 307
                                                                                                SerPhePheThrHisArgPheGlyHisHisValProValHisIleHisIleLeuLeuAla 287
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105
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133
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
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Mismatches:
Indels:
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JAPELICANT: RONDEL ET Al.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADERES:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential plaza, Suite 4900
CIPY: Chicago
STATE: IL
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Matches:
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APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: 7494
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELERAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/08748506
; Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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423.50
52.00%
35.00%
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TYPE: nucleic acid
STRANDEDNESS: double
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550 TTCTGTGACCTTCCACCTCTCCTGGGACTTGCCTGTGGAGGTACATCCCAAAACGAGGCT 609
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Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REPERENCE/DOCKET NUMBER: 74940
TELEPHONE: 312-616-5600
TELEPHONE: 312-616-5700
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                              1.58e-40
424.00
51.61%
34.41%
24.68%
                                                                                                                                                                                                                                                LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity:
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                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REPERENCE/DOCKET NUMBER: 74940
TELEPHONE: 312-616-5600
TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                               information information information for SEQ ID No: 6: SEQUENCE CHARACTERISTICS: LENGTH: 966 base pairs if TYPE: nucleic acid STRANDEDNESS: double if TOPOLOGY: linear information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information information informat
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Best Local Similarity:
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                                                                    ThrValProLysLeuLeuAlallePheTrpCysGlyAlaGlyHisileSerAlaSerAla 106
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TGTGCCTCACAGAIGTTCTTCATATTCTTTGGTATAACTGAGTGCTGCCTATTGGCA 366
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ThrAspThrIleIleAlaHisIleGlyValAlaAlaValValArgGlySerLeuLeuMet
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
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Sequence 6, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
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ZIP: 60601-6780
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                     147 ThraspThrileIleAlaHisIleGlyValAlaAlaValValArgGlySerLeuLeuMet 166
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                          127 GTATCACTAACAGGAAATGCTCTCATAAGCCCTTGCTATTTGTACCAGTCCATCTACACA 186
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547 TTCTTCTGTGATCTTCCACCTCTCGGCACTTGCCTGTGGTGATACATCCCAAATTGAG
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                                                                                       LysProValTyrLeuPheLeuCysMetLeuSerThrIleAspLeuAlaAlaSerValSer
47 AlaThrileValGlyAsnIleThrileLeuValValValAlaThrGluProValLeuHis
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Selihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
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PALO ALTO
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COUNTRY: USA
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US-09-016-434-1413
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                      AlaLeuGlyThrCysGlySerHisValCysVallleLeulleSerTyrThrProAlaLeu 266
                                                                                           PheSerPhePheThrHisArgPheGlyHisHisValProValHisIleHisIleLeuLeu 286
                                                                                                                                                         AlaAsnValTyrLeuLeuLeuProProAlaLeuAsnProValValTyrGlyValLysThr 306
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1138
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APPLICATION NUMBER: US/08/748,506 FILING DATE: 08-NOV-1996
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ronnett et al.
TITLE OF INTENTION: NOVEL SPERM RECEPTORS
UNUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite (
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08748506
Patent No. 6159707
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410.50
50.69%
34,14%
23,89%
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TYPE: nucleic acid
STRANDEDNESS: double
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CICTCCTGCTCCAGCACCCAATCAGTGCTGCTGTTTTTGCTGTGGGTTTTATAATG 785
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                                                                                                                                                        217 IleglyValAspLeuPheCysIleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeu
                                                                                     LeuAlaCysGlyAspThrArgProAsnArgValTyrGlyLeuThrAlaAlaLeuLeuVal
                                                                                                                                                                                                                               237 ArgLeuSerSerHisGluAlaArgSerLysAlaLeuGlyThrCysGlySerHisValCys
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OTHER INFORMATION: human breast cancer amplified G-protein coupled
OTHER INFORMATION: receptor 3 (BCA-GPCR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Powers, Scott
APPLICANT: Vang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
FILE REPERENCE: 018781-004720US
CURRENT APPLICATION NUMBER: US,09/546,986A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US,09/524,730
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101
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/09546986A; Patent No. 6635741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.21e-38
410.00
48.62%
31.08%
23.86%
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 1351
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 GCAGCTGTCTTGGTGGAGCCCAAACTCCACACCCCCATGTACTTCTTCCTGGGGAACCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATE: PC DS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                              ns
                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1413:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.12e-38
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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51.00%
32.33%
23.86%
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CLONE: g516319
US-09-016-434-1413
                                                                                                                                                                                                     FILING DATE:
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Query Match:
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           AspLeuAlaAlaSerValSerThrValProLysLeuAlaIlePheTrpCysGlyAla 99
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GCCCGGGCCGTGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGT
ProvalCysGlyLeuGlyThrAlaThrIleValGlyAsnIleThrIleLeuValValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NO. 6638733el G-Protein Coupled Receptors FILE REFERENCE: 018781-004710US CURRENT APPLICATION NUMBER: US/09/524,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932 CCAGCCAAGAGCACCTCCCATGAGCAGGCAAG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09524730; Patent No. 663873; GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Tularik Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1028 AACACGGAGGTGAAG 1042
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US-09-524-730-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 GAAGTCTTTGTCCTCGTGGGCTTCTCCGCACGACCTCACTAGAAACTGTCCTTCATA
                                                                                                                                                            INFORMATION: human breast cancer amplified G-protein coupled INFORMATION: receptor 3 (BCA-GPCR-3)
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Matches:
Conservative:
Mismatches:
Indels:
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 2000-03-14
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410.00
48.62%
31.08%
23.86%
CURRENT FILING DATE: 200 NUMBER OF SEQ ID NOS: 16 SOFTWARE: Patentin Ver. SEQ ID NO 5
                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                 TYPE: DNA
ORGANISM: HOMO E
FEATURE:
NAME/KEY: CDS
                                                                                                                                                    (86
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                                                                    LENGTH: 1351
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

August 27, 2004, 18:28:44; Search time 3045 Seconds (without alignments) 3226.488 Million cell updates/sec Run on:

1718 1 MSSTLGHNMESPHHTDVDPS......RKRVVRVFQSGQGMGIKASE 329 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-10-081-775-2 **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

55026578 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

em_estba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Res i	esult No.	Score	Query Match	Length	DB	ID	Description	
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ALIGNMENTS

AY401474 948 bp DNA linear GSS 12-DEC-2003 Mus musculus HCM0902 gene, VIRTUAL TRANSCRIPT, partial sequence, AY401474 AY401474.1 GI:39757463 genomic survey sequence ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION RESULT 1 AY401474

GSS.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 948)

REFERENCE

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948 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM0902 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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1 (bases 1 to 94).

1 (Catk, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
CysGluHisMetAlaValValLysLeuAlaCysGlyAspThrArgProAsnArgValTyr
                                                                                                                                                                                          AlaLeuIleAlaGlnAlaValLeuArgLeuSerSerHisGluAlaArgSerLysAlaLeu
                                                                                                                                                                                                                                                                                                                 PhepherhrisArgPheGlyHisHisValProValHisIleHisIleLeuLeuAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                             GlyLeuThrAlaAlaLeuLeuValIleGlyValAspLeuPheCysIleGlyLeuSerTyr
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178
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Matches:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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          Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Line and Cargill, M. Line and Cargill, M. Line and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and Cargill, M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. D. and M. A. and M. A. and M. A. and M. A. and M. A. and M. A. and M. and M. A. and M. A. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and M. and
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Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.

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Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases I to 936)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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ATCTGGGATGGGGCCCTCCGGCTTCTGAAGTGGGGC 933
  Indels:
             Gaps:
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                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clases 1 to 936)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 HisAsnMetGluSerProHisHisThrAspValAspProSerValPhePheLeuLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 IleProGlyLeuGluGlnPheHisLeuTrpLeuSerLeuProValCysGlyLeuGlyThr
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Conservative:
Mismatches:
Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
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<1. . . >936
/locus_tag="HCM0904"
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AY401478 936 bp DNA linear GSS 12-DEC-2003 Homo sapiens HCM0904 gene, VIRTUAL TRANSCRIPT, partial sequence,

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ValTyrLeuLeuLeuProProAlaLeuAsnProValValTyrGlyValLysThrLysGln 308
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Mismatches:
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                                 Inferring nonneutral evolution from human-chimp-mouse orthologous
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Catarrhini; Hominidae; Pan.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pan troglodytes
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleoston
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleoston
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
1 (bases 1 to 948)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                          ThrTyrCysGluHisMetAlaValValLysLeuAlaCysGlyAspThrArgProAsnArg
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
                  ThraspThr11e11eAlaHisIleGlyValAlaAlaValValArgGlySerLeuLeuMet
                                                                       LeuProCysProPhePheIleGlyArgLeuAsnPheCysGlnSerHisValIleLeuHis
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genomic survey sequence.
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JOURNAL
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AUTHORS
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274 GCTGGTGAGATTTCCTTTGGTGGATGCCTGGCCCAGATGTTTTGTGTCCATTCTATTGT 333
                                                                                                                                                                                                                       454 CTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTTCTTGCTGAGGCGACTCCCCTAC 513
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mus musculus HCM5153 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                                                       159 ValValArgGlySerLeuLeuMetLeuProCysProPhePheIleGlyArgLeuAsnPhe
                                                                                                                                                 394 CCATTAAGGTATACAACCATTCTCAACCATGCTGTCATAGGCAGAATTGGCTTTTGTTGGG
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                                                                                                                                                                                                                                                                                                                                                                       239 SerSerHisGluAlaArgSerLysAlaLeuGlyThrCysGlySerHisValCysVallle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               694 CCATCTCATGATGCCCAGCACAAGCTCTGAGTACCTGTGGCTCCCACATTGGCATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysGlnSerHisVallleLeuHisThrTyrCysGluHisMetAlaValValLysLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                     219 ValAspLeuPheCysIleGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 954)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
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Mus musculus
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                                                                                                           Homo sapiens HCM5153 gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 ATCCCTTTCTGTGCCATGTATCTTGTAGCACTGGTTGGAAATGCTGCCCTCATCCTGGTC 153
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 957)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Tanenbaum,D.M., Civello,B., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, W.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 CCAGACACCTTCTTCTTAACAGGGATCCCAGGGCTGGAGGCTGCCCACTTCTGGATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuProValCysGlyLeuGlyThrAlaThrIleValGlyAsnIleThrIleLeuValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 IleArgLysArgValValArgValPheGlnSerGly 320
                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Science 302 (5652), 1960-1963 (2003)
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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889.50
69.41%
52.63%
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DB:
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936 bp DNA linear GSS 12-DEC-2003
Mus musculus HCM0904 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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                                                                                                            27 ileproglyLeuGluGlnPheHisLeuTrpLeuSerLeuProValCysGlyLeuGlyThr 46
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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751 CIGGITITCIAIAIACCIGCITICITCITCICCITCCICACCCAICGCITIGGICACAAICGA
                                               ValProValHisIleHisIleLeuLeuAlaAsnValTyrLeuLeuLeuProProAlaLeu
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163
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Mismatches:
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/db_xref="taxon:10090"
<1...>936
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1. .936
                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValAlaThrGluProValLeuHisLysProValTyrLeuPheLeuCysMetLeuSerThr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 IleAspLeuAlaAlaSerValSerThrValProLysLeuLeuAlaIlePheTrpCysGly 98
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                                                                                                                                                                                                                                                                                                                                                                                                                              LeuProValCysGlyLeuGlyThrAlaThrIleValGlyAsnIleThrIleLeuValVal 58
   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Conservative:
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/mol type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM5153"
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                                                                                                                                                                                 genes
                                                                                                                                                                                                                                                                          Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Hazada,A., Yamamoto,R., Matsumoto,H., Sakaquchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikwaa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., RIKEN integrated sequence analysis (RISA) system--384-format genome Reguencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1964)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length to CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Please visit our web site for further (URL:http://genome.goc.riken.go.jp/URL:http://fantom.gsc.riken.go.jp/Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                   GAGCCCATGTTCTACTTTCTGGCCATCTTTCTTCAGCGACTTGGCTCTTTCTACAACC 234
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Sciurognathi; Muridae; Murinae; Mus.
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MOR18-2, full insert sequence.
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Mammalia; Eutheria;
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ARNA linear HTC 18-SEP-2003 Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631413D08 product:OLFACTORY RECEPTOR MOR18-2, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                 IleHisIleLeuLeuAlaAsnValTyrLeuLeuLeuProProAlaLeuAsnProValVal
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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DVYLLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDIEAGGNT"
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|||| TCTTCCAGTCCGCCCCACTTGGTCAACGATGAGTTCCTGCAACTTCACCCATGCCACC 1170
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                                                                                                                                                                                                                                                                                                                                                                                     AlaAlaSerValSerThrValProLysLeuLeuAlaIlePheTrpCysGlyAlaGlyHis 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 TyrThrProAlaLeuPheSerPhePheThrHisArgPheGlyHisHisValProValHis 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 PheCysileGlyLeuSerTyrAlaLeuIleAlaGlnAlaValLeuArgLeuSerSerHis 241
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                                                   SerSerThrLeuGlyHisAsnMetGluSerProHisHisThrAspValAspProSerVal 21
                                                                                                                                     PhePheLeuLeuGlyIleProGlyLeuGluGlnPheHisLeuTrpLeuSerLeuProVal
                                                                                                                                                                                                                     CysGlyLeuGlyThrAlaThrIleValGlyAsnIleThrIleLeuValValValAlaThr
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), inboratory for genome
Exploration Research Grup, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230 0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
WRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein id="BAC25966.1"
/db_xref="G1:26124424"
/translation="WSSCNFTHATFLLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIV
VFIVRTERSLHAPMYLFLCHMAAIDLALSTSYMPKILALFWFDSREITFDACLAQMFP
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LIKRLAFCHSNVLSHSYCVHQDVMKLAYTDTLPNVVYGLTAILLVMGVDVMFISLSYF
LIIRTVLQLPSKSERAKAFGTCVSHISVVLAFYVPLIGLSVVHRFGNSLDPIVHVLMG
                                                                                                 Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatuu, M., Hiramote, K., Hirzoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Lich, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koth, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Makamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Obsato, N., Santo, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takeda, Y., Tanaka, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Murametsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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/db_xref="FRANTO" DB:4631413D08"

/db_xref="taxon:10090"

/clone="4631413D08"

/tissue type="skin"

/clone lib="RikEN full-length enriched mouse cDNA library"

/dev_steage="0" day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                            on functional annotation
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(SPTR|AAL60674, evidence: FASTY, 100%ID, 100%length;
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Group Phase I & II Team.
Analysis of the mouse transcriptome based 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3410)
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Matches:
Conservative:
Mismatches:
Indels:
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity:
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948 bp DNA linear GSS 16-DEC-2003
Homo sapiens OR52R1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeuPheSerPhePheThrHisArgPheGlyHisHisValProValHisIleHisIle
                                                                                 165 LeuMetLeuProCysProPhePheIleGlyArgLeuAsnPheCysGlnSerHisValIle
                                                                                                                                                              LeuHisThrTyrCysGluHisMetAlaValValLysLeuAlaCysGlyAspThrArgPro
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                                                          IleLeuThrAspThrIleIleAlaHisIleGlyValAlaAlaValValArgGlySerLeu
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Andel, M. Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submitsed on Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Submisted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
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db_xref="taxon:9598"
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/gene="OR52R1"
/locus_tag="HCM3944"
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Query Match:
DB:
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Pan troglodytes OR52R1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
     1 (bases 1 to 948)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                      CysProPhePhelleGly---ArgLeuAsnPheCysGlnSerHisVallleLeuHisThr
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/mol_type="genomic DNA"
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AF101706 11086 bp DNA linear GSS 06-NOV-2000 AF101706 Human Homo sapiens genomic clone pTWB298.21SP6, genomic
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Bepler, G., O'Briant, K.C., Kim, Y.C., Schreiber, G. and Pitterle, D.M. A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOH11A metastasis suppressor
                                                                                                                                                                                                                                                TyrValAlaileCysHisProLeuArgTyrAlaThrileLeuThrAspThrileileAla
                                                                                                                                                                                                  313 TTCATCCACACCTTGTCTTTAGTGGAGTCATCGGTTCTACTGTCTATGTCCTTCGACCGC
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                         PhelleHisAlaPheCysMetMetGluSerThrValLeuLeuAlaMetAlaPheAspArg
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Box 2610, MSRB, Room 117, Durham, NC 27710, USA
part of a 1.4 megabase contig including the LOH11A metastasis
suppressor region Bin F
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Medicine and Radiology
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VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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/locus_tag="HCM2267"
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Matches:
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